

Delaval, Jan

73287

From: Gambel, Phillip
Sent: Wednesday, August 14, 2002 9:59 AM
To: Delaval, Jan
Subject: 09 / 811384

jan

please perform a sequence and a sequence interference search for
09 / 811384

SEQ ID NO: 10

SEQ ID NO: 11

thanx

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art unit 1644
308-3997

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1644 maiblox 9e12

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SEARCH REQUEST FORM

Scientific and Technical Information Center

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If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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Searcher: Jan

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Searcher Location: _____

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Type of Search

NA Sequence (#) _____

AA Sequence (#) ☒

Structure (#) _____

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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:59:25 ; Search time 29.5 seconds

(without alignments)
755.686 Million cell updates/sec

Title: US-09-811-384-10

Perfect score: 1233

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....PSNTKVDKKVEPKSCDKTHT 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.71.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787	63.8	241	2 S69131	Ig heavy chain (DO
2	782.5	63.5	220	2 A49444	Ig gamma-1 heavy c
3	693.5	56.2	444	2 P24436	monoclonal antibod
4	688	55.8	246	2 S38950	Ig gamma chain - m
5	688	55.8	446	2 S40295	Ig gamma-2a chain
6	683.5	55.4	469	2 S37483	Ig gamma-2a chain
7	680.5	55.2	220	2 S68211	Ig heavy chain (Ma
8	670.5	54.4	474	1 G2MS11	Ig gamma-2b chain
9	665	53.9	213	2 S68213	Ig heavy chain (Ma
10	664.5	53.9	548	2 S38864	Ig epsilon chain C
11	662.5	53.7	214	2 P24202	monoclonal antibod
12	651	52.8	221	2 S49220	Ig gamma-1 chain -
13	635	51.5	475	2 S01321	Ig gamma-2b chain
14	630	51.1	231	2 P24155	Ig gamma-2b chain
15	614.5	49.8	470	2 S22080	Ig heavy chain pre
16	604	49.0	254	2 B31790	Ig heavy chain v r
17	580	47.0	549	2 S04845	Ig heavy chain pre
18	578	46.9	472	2 S31459	Ig gamma-1 chain -
19	563	45.7	330	1 GHU	Ig gamma-1 chain C
20	517.5	42.0	143	2 S23624	Ig heavy chain v r
21	508	41.2	171	2 S23623	Ig heavy chain v r
22	505.5	41.0	377	2 A60764	Ig gamma-3 chain C
23	505.5	41.0	377	2 A23511	Ig gamma-3 chain C
24	490	39.7	97	2 S26652	Ig gamma-1 chain C
25	489	39.7	627	2 S14683	Ig mu chain precu
26	479	38.8	585	2 A46507	Ig alpha chain - c
27	475	38.5	326	1 G2HU	Ig gamma-2 chain C
28	474	38.4	327	1 G4HU	Ig gamma-4 chain C
29	470	38.1	288	2 S29690	Ig heavy chain VDJ

30 467.5 37.9 249 2 S69340 Ig heavy chain VHI
31 463 37.6 572 2 B46529 Ig y heavy chain (
32 451.5 36.6 509 2 S17597 Ig delta chain (WI
33 448 36.3 218 2 A36040 Ig heavy chain v-I
34 445 36.1 170 2 A35944 Ig gamma-2a chain
35 445 36.1 342 2 A46529 Ig gamma chain (5.
36 438.5 35.6 160 2 S05271 Ig heavy chain pre
37 434.5 35.2 119 2 S31107 Ig heavy chain - h
38 431 35.0 147 2 S37780 Ig variable region
39 426.5 34.6 134 2 S31699 Ig heavy chain v r
40 423 34.3 120 2 S48798 Ig heavy chain v r
41 423 34.3 128 2 I37267 Ig heavy chain v r
42 421 34.1 124 2 S20782 Ig heavy chain v r
43 420.5 34.1 119 2 C36005 Ig heavy chain v r
44 419.5 34.0 125 2 S30531 Ig heavy chain v r
45 418.5 33.9 138 2 S31666 Ig heavy chain v r

ALIGNMENTS

RESULT 1
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin IgG Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobul
A:Reference number: S69130; MUID:95255298
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <SPO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 63.8%; Score 787; DB 2; Length 241;
Best Local Similarity 67.8%; Pred. No. 8.8e-48;
Matches 154; Conservative 22; Mismatches 47; Indels 4; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETVTHWMRQAPGKGLWVAGINPKNGTSH 60
Db 1 QVQLVQSGVERKVPQSVRIKSKASGYAFENYIHWRQAPGKGLWVAGINPVAGAVS- 59
QY 61 NORFMDRFTISVDKSTSTAYMOMNSLRAEDTAVYYCARWGLNTGFDVRYFDVMGQGTFLV 120
Db 60 SEKFRDLVNSSDPTSAITVSNQNLRLSRDSDTGRYFCAR---VSYDFSQYGMVWGQGTTV 116
QY 121 TVSSASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 180
Db 117 IVSSASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 176
QY 181 LQSSGLYSLSWVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC 227
Db 177 LQSSGLYSLSWVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC 223

RESULT 2
A49444
Ig gamma-1 heavy chain (New) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C:Accession: A49444
R:Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A
A:Reference number: A49444; MUID:93066153


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Best Local Similarity 57.8%; Pred. No. 1.2e-40;
Matches 130; Conservative 41; Mismatches 46; Indels 8; Gaps 3;

Qy 1 EVLVESGGLVOPGSLRLSCATSGYTFEYTHMWMRQAPGKLEWAGINPKNGTSH 60
Db 1 QIQLQSGPGLVPRGASVKISCKASGYTFDYIHWKVRPGEGLEWIGWYPCSGNTKY 60
Qy 61 NQRFMDRFTISVDKSTSTAYMWNLSRAEDTAVYYCARWRGLNGYGFVDFVWGQGLV 120
Db 61 NKFNGKATLTVDTSSTAYMQLSSLTSEDYVYFCA--RGGKFA-----MDYWGQGLV 113
Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 114 TVSSAKTTPSYVPLAPVCGDTGSSVTLGCLVKGYFPEPTLTWNSGSLSSGVHTFPAV 173
Qy 181 LOSGGLYSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPK 225
Db 174 LQSD-LYTLSSVTVTSTWPSQSITCNVAHPASSTKVDKKIEPR 217

RESULT 6
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 55.4%; Score 683.5; DB 2; Length 469;
Best Local Similarity 56.9%; Pred. No. 2.6e-40;
Matches 128; Conservative 41; Mismatches 51; Indels 5; Gaps 2;

Qy 1 EVLVESGGLVOPGSLRLSCATSGYTFEYTHMWMRQAPGKLEWAGINPKNGTSH 60
Db 20 QIQLQSGPGLVPRGASVKISCKASGYTFDYIHWKVRPGEGLEWIGWYPCSGNTKY 79
Qy 61 NQRFMDRFTISVDKSTSTAYMWNLSRAEDTAVYYCARWRGLNGYGFVDFVWGQGLV 120
Db 80 NENFKGKATLTVDTSSTAYMQLSSLTSEDYVYFCARANGAT---ATLLDYWGQGLT 135
Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 136 TVSSAKTTPSYVPLAPVCGDTGSSVTLGCLVKGYFPEPTLTWNSGSLSSGVHTFPAV 195
Qy 181 LOSGGLYSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPK 225
Db 196 LQSD-LYTLSSVTVTSTWPSQSITCNVAHPASSTKVDKKIEPR 239

RESULT 7
Ig heavy chain (Mab13-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C:Accession: S68211
R: Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.;
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223
A:Accession: S68211
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
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A:Residues: 1-220 <TAK>
A:Cross-references: EMBL:D29669; NID:g473958; PIDN:BAA06140.1; PID:g473959
A:Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequen
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:136-200/Domain: immunoglobulin homology <IMM>

Query Match 55.2%; Score 680.5; DB 2; Length 220;
Best Local Similarity 59.9%; Pred. No. 2e-40;
Matches 136; Conservative 24; Mismatches 54; Indels 13; Gaps 4;

Qy 5 VESGGLVOPGSLRLSCATSGYTFEYTHMWMRQAPGKLEWAGINPK--NGGTSHQ 62
Db 1 LESGGLVPRGNSLKLCLTSGTFESNRMHLRQPPGKRLEWIAVITVKSNDYGAKE 60
Qy 63 RFMDRFTISVDKSTSTAYMWNLSRAEDTAVYYCAR--WRGLNGYGFVDFVWGQGLV 120
Db 61 SVRGFTISRDDSKSVYLQNMRLREEDTATVYCCRTPW-----VYAMDCWGQGLSV 112
Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 113 TVSSAKTTPSYVPLAPGSAQTNSMVTGLCLVKGYFPEPTVTVWNSGSLSSGVHTFPAV 172
Qy 181 LOSGGLYSSVVTVPSSSLGTQYICNVNHPKSTNTKVDKKVEPKSC 227
Db 173 LQSD-LYTLSSVTVPSSSTWTFSETVTCNVAHPASSTKVDKKIIVPRDC 218

RESULT 8
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A26235; A26232; A26233; A53598
R: Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
R: Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro
A:Reference number: A02157; MUID:80120716
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A:Note: the sequence was determined from the germline gene
R: Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b
A:Reference number: A26235; MUID:80081501
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A:Note: Lys-474 is probably removed posttranslationally
R: Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno
A:Reference number: A26232; MUID:80081502
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
R: Ojito, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g
A:Reference number: A26233; MUID:82173203
```

A;Contents: b allele
A;Accession: A26233
A;Molecule type: DNA
A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A;Cross-references: GB:J00461
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A;Reference number: A53598; MUID:94216359
A;Accession: A53598
A;Status: preliminary
A;Molecule type: protein
A;Residues: 234-251 <IM>
C;Comment: The a allele sequence is shown.
C;Genetics:
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.4%; Score 670.5; DB 1; Length 474;
Best Local Similarity 53.3%; Pred. No. 2.1e-39;
Matches 129; Conservative 37; Mismatches 57; Indels 19; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLVWVAGINPKNGTSH 60
Db 20 EVQLQSGDELVPAGSVKMKSCRASGYTFYTHMWRQAPGQGLWIGVINPKNGTGF 79
QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYDVMQGQTLV 120
Db 80 NERFKGATLTSDKSSNTAYMELSSLTSEDSAVYICAR---DYDYD--WFAYWQGQTLV 133
QY 121 TVSSASTKGSPVPLAPSSKSTGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAP 180
Db 134 TVSAAKTTPPSVYPLAPGCGDTTGSSTVSGCLVKGYFPESVTVTWNSGSLSSVHTLSQA 193
QY 181 LQSGGLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKKVEP-----KSC 227
Db 194 LQSGGLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVDDKKLEPSGPSTINPCPKCEC 253
QY 228 DK 229
Db 254 HK 255

RESULT 9
S68213
Ig heavy chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jan-2000
C;Accession: S68213
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T. FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223
A;Accession: S68213
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-213 <TAK>
A;Cross-references: EMBL:D29667
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;137-201/Domain: immunoglobulin homology <IM>

Query Match 53.9%; Score 665; DB 2; Length 213;
Best Local Similarity 60.2%; Pred. No. 2.3e-39;
Matches 133; Conservative 28; Mismatches 50; Indels 10; Gaps 3;

QY 2 VOLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLVWVAGINPKNGTSHN 61
Db 2 VOLVESGGGLVQPGGSRKLSCAASGFTTSSFGMHWVRQAPKEKGLWVAYISGSSSIYYA 61
QY 62 QRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICAR-WRGLNYGFDVRYDVMQGQTLV 120
Db 62 DTVKGRFTISRDNPKNTLFLQMTSLRSEDATMYICARSW-----LLPFDYWGQGTLL 113
QY 121 TVSSASTKGSPVPLAPSSKSTGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAP 180
Db 114 TVSSAKTTPPSVYPLAPGCGDTTGSSTVSGCLVKGYFPESVTVTWNSGSLSSVHTFPAL 173
QY 181 LQSGGLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKK 221
Db 174 LQ-SGLYTMSSSVTVPSSTWPSQTVCVAHPASSTTVDDK 213

RESULT 10
S38864
Ig epsilon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of
A;Reference number: S38864
A;Accession: S38864
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-548 <KIP>
A;Cross-references: EMBL:227397; NID:9416537; PIDN:CAA81788.1; PID:940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 53.9%; Score 664.5; DB 2; Length 548;
Best Local Similarity 58.6%; Pred. No. 6.4e-39;
Matches 133; Conservative 34; Mismatches 55; Indels 5; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLVWVAGINPKNGTSH 60
Db 1 QVKLESGLDLVKPGGSLKLSCAASGLTFSYGMHWVRQIPDKRLWVATISSGGTYIYY 60
QY 61 NORFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYDVMQGQTLV 120
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDATMYICAR-QGVSV---TMRFAYWQGQTLV 116
QY 121 TVSSASTKGSPVPLAPSSKSTGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAP 180
Db 117 TVSAGKTTTPPSVYPLAPGSAAGTNSMVTLGCLVKGYFPESVTVTWNSGSLSSVHTFPAP 176
QY 181 LQSGGLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKKVEPKSC 227
Db 177 LQSD-LYTLSSSVTVPSSTWPSSTWPSQTVCVAHPASSTKVDKKIVPRDC 222

RESULT 11
PC4202
monoclonal antibody Maba34 gamma1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 21-Jan-2000
C;Accession: PC4202
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H. Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A;Reference number: PC4202; MUID:97082978
A;Accession: PC4202

A:Molecule type: mRNA
A:Residues: 1-214 <KWA>
A:Cross-references: GB:U29146; NID:g1594223; PIDN:AAC52820.1; PID:g1594224
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-214/Domain: C region #status predicted <CRG>
F:132-196/Domain: immunoglobulin homology <IMM>

Query Match 53.7%; Score 662.5; DB 2; Length 214;
Best Local Similarity 55.5%; Pred. No. 3.4e-39;
Matches 126; Conservative 36; Mismatches 52; Indels 13; Gaps 2;

QY 1 EVLVESGGGLVQPGSLRLSCATSGYTFEYTHMMRQAPKGLWVAGINPKNGTSH 60
DB 1 EVLVESGAELMKPGASVKISKATDYFESSYWIWKQRPQHGLEWIGDILPGSGNTY 60
QY 61 NORFMDRTTISVDKSTSTAYQMNSLRADTAIVYCARWGLNYGFDVRYFDVWGQGLV 120
DB 61 NERFKGATFTADTSSNTAYMQLSLTSEDSAVYCA-----IPDYWGQGTTL 108
QY 121 TVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 180
DB 109 TVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPTVWNSGSLSSGVHTFP 168
QY 181 LQSSGLYSLSSVTVPPSSLTGTQTYICNVNHPKNTKVDKVEPKSC 227
DB 169 LQSD-LYTLSSSVTVPPSRPSETVTCNVHPASSTKVDKIVPRDC 214

RESULT 12
S49220
Ig gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R:Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <KIP>
A:Cross-references: EMBL:237502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A:Experimental source: strain Balb/c
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-120/Domain: V region #status predicted <VRG>
F:121-221/Domain: C region #status predicted <CRG>
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 52.8%; Score 651; DB 2; Length 221;
Best Local Similarity 55.9%; Pred. No. 2.2e-38;
Matches 127; Conservative 37; Mismatches 57; Indels 6; Gaps 4;

QY 1 EVLVESGGGLVQPGSLRLSCATSGYTFEYTHMMRQAPKGLWVAGINPKNGTSH 60
DB 1 QVKLESAGELVKSGASVKLSCTASGFNKTDMYMHVVKORPEQGLEWIGRIDPANGEIKY 60
QY 61 NORFMDRTTISVDKSTSTAYQMNSLRADTAIVYCARWGLNYGFDVRYFDVWGQGLV 120
DB 61 DPKFGQTATITADTSTNTAYQLSLTSEDTAVYICVR-RG--YGSSQEPY--WGQGTTL 115
QY 121 TVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 180
DB 116 TVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPTVWNSGSLSSGVHTFP 175
QY 181 LQSSGLYSLSSVTVPPSSLTGTQTYICNVNHPKNTKVDKVEPKSC 227
DB 176 LQSD-LYTLSSSVTVPPSSWTPESTVTCNVHPASSTKVDKIVPRDC 221

RESULT 13
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe
A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475 <DE1>
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 51.5%; Score 635; DB 2; Length 475;
Best Local Similarity 51.7%; Pred. No. 6.2e-37;
Matches 125; Conservative 41; Mismatches 58; Indels 18; Gaps 3;

QY 1 EVLVESGGGLVQPGSLRLSCATSGYTFEYTHMMRQAPKGLWVAGINPKNGTSH 60
DB 20 QVQLQSGAELARPGASVKLSKASGVTLTSGISWVKORTGGGLEWIGEIVPGSGNSYF 79
QY 61 NORFMDRTTISVDKSTSTAYQMNSLRADTAIVYCARWGLNYGFDVRYFDVWGQGLV 120
DB 80 NEKFKGATLTVDKSSSTAYLHLSLTSEDSAVYFCAGPRQVG----LLPFGYWGQGLV 135
QY 121 TVSSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFP 180
DB 136 TASAATTPPSVYPLAPGCGDTTGGSSVTLGCLVKGYFPEPTVWNSGSLSSVHTFP 195
QY 181 LQSSGLYSLSSVTVPPSSLTGTQTYICNVNHPKNTKVDKVEP-----KSC 227
DB 196 LQ-SGLYTMSSVTVPPSSWTPESTVTCNVHPASSTTVDDKLEPSGPTSTINPCPCKEC 254
QY 228 DK 229
DB 255 HK 256

RESULT 14
PC4155
Ig gamma-2b chain V-C region MabB23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C:Accession: PC4155
R:Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 189, 237-239, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A:Reference number: PC4155; MUID:96194809
A:Accession: PC4155
A:Molecule type: mRNA
A:Residues: 1-231 <KWA>
A:Cross-references: GB:U28970; NID:g1262180; PIDN:AAC52489.1; PID:g1262181
A:Note: This protein has unusual amino acid compared with the conserved sequences of
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-231/Product: heavy chain #status predicted <MAT>
F:98-102/Region: unique D sequence
F:103-119/Region: V region
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 51.1%; Score 630; DB 2; Length 231;
Best Local Similarity 54.3%; Pred. No. 6.6e-37;
Matches 125; Conservative 32; Mismatches 55; Indels 18; Gaps 4;

QY	1	EVQLVESGGGLVQPGGSLRLSCA	SGYTFTEYTMHMRQAPGKLEWVAGINPKNGCTSH	60
Db	1	EVQLVESGGGLVQPGGSLRLSCA	SGYTFTEYTMHMRQAPGKLEWVAGINPKNGCTSH	59
QY	61	NOREMDREFTISVDKSTSTAYM	QMNLSRAEDTAVYYCAR-----WRGLNYGFDVRYFDWM	114
Db	60	NSALKSRLSINKDNKSKQVFLK	MNSLHDDTAMYYCVKHEDRYDW-----YFDWM	109
QY	115	GGTLVTVSSASTKGPSVFPLAP	SKSTSGGTAALGCLVKDYKDPPEPTVTSWNSGALTSGV	174
Db	110	GAGTTVTVSSAKTTPSPVPLA	PRCGDGTSSVTLGCLVKGYFPESTVITWNSGSLSSV	169
QY	175	HTFPAVLOSSGLYSLSSVVTVP	SSSLGTTQTYICNVNHHKPSNTKVDKKVEP	224
Db	170	HTFPALQ--SGLYTMSSSVTP	SPSWPQOTVTCVAHPASSTVVDKKLEP	218
RESULT 15				
S22080				
Ig heavy chain precursor (B/MF 4A.17 H5.A5) - bovine				
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)				
C:Species: Bos primigenius taurus (cattle)				
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999				
C:Accession: S22080; S06610; A31303				
R:Sanders, P.G.				
submitted to the EMBL Data Library, November 1991				
A:Reference number: S22080				
A:Accession: S22080				
A>Status: preliminary				
A:Molecule type: mRNA				
A:Residues: 1-470 <S>				
A:Cross-references: EMBL:X62916; NID:q439; PIDN:CAA44699.1; PID:q440				
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.				
Mol. Immunol. 26, 841-850, 1989				
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma				
A:Reference number: S06610; MUID:90097956				
A:Accession: S06610				
A:Molecule type: DNA				
A:Residues: 142-470 <SYM>				
A:Cross-references: EMBL:X16701				
A:Note: the sequence was determined from the germline gene				
C:Genetics:				
A:Gene: Ig CH gamma-1				
R:Introns: 98/1; 111/1; 221/1				
C:Superfamily: immunoglobulin C region; immunoglobulin homology				
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein				
F:161-225/Domain: immunoglobulin homology <IM>				
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted				
Query Match 49.8%; Score 614.5; DB 2; Length 470;				
Best Local Similarity 54.9%; Pred. No. 1.6e-35;				
Matches 129; Conservative 27; Mismatches 66; Indels 13; Gaps				
QY	1	EVQLVESGGGLVQPGGSLRLSCA	SGYTFTEYTMHMRQAPGKLEWVAGINPKNGGTS-	59
Db	20	QVQLRESGPSLVKPSQTLSTCT	VSGLSSVYALTVWRQAPGKLEWVGGIT--SGGTTY	77
QY	60	HNQRFMDREFTISVDKSTSTAY	MNLSRAEDTAVYYCARWGRGLNYG--FDVRYFDVWGQG	117
Db	78	YNPALKSRLSITKENSQVSLVS	SVTPEDTATYYCAR---STYGEVGDGAIADAWGQG	134
QY	118	TLVTVSSASTKGPSVFPLAP	SKSTSGGTAALGCLVKDYKDPPEPTVTSWNSGALTSGVHTF	177
Db	135	LLVTVSSASTAPKVPYPLSS	CCGDKSSSTVTLGCLVSSYMPPEPTVITWNSGALKSGVHTF	194
QY	178	PAVLOSSGLYSLSSVVTVPSS	SLGTTQTYICNVNHHKPSNTKVDKKVE-----PKSCD	228
Db	195	PAVLQSSGLYSLSSMTVP	GGTSG--QTFTCNVAHPASSTKVDKAVDPTCKPSPCD	248

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OM protein - protein search, using sw model

Run on: August 14, 2002, 11:01:15 ; Search time 16.05 seconds
(without alignments)
559.684 Million cell updates/sec

Title: US-09-811-384-10

Perfect score: 1233

Sequence: 1 EVQVSGGLVPGGSLRL.....PSNTKVDKVKPKSCDKTHT 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	563	45.7	330	1	GCL_HUMAN
2	475	38.5	326	1	G2_HUMAN
3	474	38.4	327	1	G2_HUMAN
4	416	33.7	120	1	HV50_MOUSE
5	405.5	32.9	117	1	HV12_MOUSE
6	405.5	32.9	117	1	HV13_MOUSE
7	399	32.4	122	1	HV3G_HUMAN
8	395	32.0	118	1	HV51_MOUSE
9	392	31.8	137	1	HV11_MOUSE
10	392	31.8	139	1	HV07_MOUSE
11	391	31.7	122	1	HV21_MOUSE
12	384	31.1	122	1	HV20_MOUSE
13	382	31.0	119	1	HV38_MOUSE
14	380.5	30.9	115	1	HV3D_HUMAN
15	380.5	30.9	123	1	HV18_MOUSE
16	379.5	30.8	123	1	HV19_MOUSE
17	379.5	30.8	123	1	HV25_MOUSE
18	377.5	30.6	117	1	HV17_MOUSE
19	377.5	30.6	123	1	HV23_MOUSE
20	376.5	30.5	121	1	HV32_MOUSE
21	375.5	30.5	123	1	HV22_MOUSE
22	374.5	30.4	119	1	HV31_HUMAN
23	373.5	30.3	142	1	HV01_RAT
24	371	30.1	136	1	HV16_MOUSE
25	371	30.0	119	1	HV37_MOUSE
26	369.5	30.0	120	1	HV03_MOUSE
27	369	29.9	119	1	HV40_MOUSE
28	369	29.9	120	1	HV3U_HUMAN
29	368.5	29.8	123	1	HV24_MOUSE
30	367.5	29.8	120	1	HV3E_HUMAN
31	367.5	29.8	144	1	HV26_MOUSE
32	365	29.6	114	1	HV1C_CANFA
33	365	29.6	147	1	HV1C_HUMAN

ALIGNMENTS

RESULT 1	GCL_HUMAN	117	1	HV3C_HUMAN	117	1	P01764
ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.			homo sapien
AC	P01857;						P01769
DT	21-JUL-1986 (Rel. 01, Created)						homo sapien
DT	21-JUL-1986 (Rel. 01, Last sequence update)						P01746
DT	16-OCT-2001 (Rel. 40, Last annotation update)						mus musculus
DE	Ig gamma-1 chain C region.						P01776
GN	IGHG1.						homo sapien
OS	Homo sapiens (Human).						P01781
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						homo sapien
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						P01809
OX	NCBI_TaxID=9606;						mus musculus
RN	[1]						P03980
RP	SEQUENCE FROM N.A.						mus musculus
RX	MEDLINE=82274238; PubMed=6287432;						P01763
RA	Ellison J.W., Berson B.J., Hood L.E.;						homo sapien
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."						P01811
RL	Nucleic Acids Res. 10:4071-4079(1982).						mus musculus
RN	[2]						P01799
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).						mus musculus
RX	MEDLINE=71064024; PubMed=5489771;						P01801
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,						
RT	Waxdal M.J., Edelman G.M.;						
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."						
RN	[3]						
RP	SEQUENCE OF 136-329 (EU).						
RX	MEDLINE=71064025; PubMed=5530842;						
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,						
RT	Edelman G.M.;						
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."						
RN	[4]						
RP	SEQUENCE (MYELOMA PROTEIN NIE).						
RX	MEDLINE=77070269; PubMed=826475;						
RA	Ponstingl H., Hilschmann N.;						
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."						
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).						
RN	[5]						
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.						
RX	MEDLINE=83289131; PubMed=6884994;						
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;						
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."						
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).						
RN	[6]						
RP	DISULFIDE BONDS.						
RX	MEDLINE=71064027; PubMed=4923144;						
RA	Gall W.E., Edelman G.M.;						
RT	"The covalent structure of a human gamma G-immunoglobulin. X.						

RT Intrachain disulfide bonds. ";
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges. ";
 RT Hoppe-Seyler's z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.;
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution. ";
 RL Biochemistry 20:2361-2370(1981).
 CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
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 DR PIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; .
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_like; 1.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure.
 FT NON_TER 1
 FT DOMAIN 1
 FT DOMAIN 99
 FT DOMAIN 111
 FT DOMAIN 224
 FT DISULFID 27
 FT DISULFID 103
 FT DISULFID 109
 FT DISULFID 112
 FT DISULFID 144
 FT DISULFID 250
 FT CARBOHYD 180
 FT MOD_RES 330
 FT VARIANT 97
 FT VARIANT 239
 FT VARIANT 241
 FT STRAND 123
 FT HELIX 130
 CH1.
 HINGE.
 CH2.
 CH3.
 INTERCHAIN (WITH LIGHT CHAIN).
 INTERCHAIN (WITH HEAVY CHAIN).
 N-LINKED (GLCNAC. . .).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GIM(3) MARKER).
 /FTid=VAR_003886.
 D -> E (IN GIM(NON-1) MARKER).
 /FTid=VAR_003887.
 L -> M (IN GIM(NON-1) MARKER).
 /FTid=VAR_003888.

FT TURN 136 137
 FT STRAND 141 148
 FT STRAND 158 162
 FT TURN 163 164
 FT STRAND 165 166
 FT STRAND 175 178
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 206
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 240
 FT TURN 241 242
 FT STRAND 245 256
 FT STRAND 260 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT STRAND 302 303
 FT STRAND 306 312
 FT TURN 313 314
 FT TURN 316 317
 FT STRAND 320 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 45.7%; Score 563; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.8e-41;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 125 ASKKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 184
 Db 1 ASKKGPSVFLPLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
 QY 185 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHT 232
 Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHT 108
 RESULT 2
 ID GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-2 chain C region.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RX MEDLINE=82197621; PubMed=6804948;
 RA Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RT heavy chain constant region genes. ";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaigo T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: implications for
 RT evolution of a gene family. ";
 RL Cell 29:671-679(1982).

[3] SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RP TISSUE-Fetal liver;
 RC MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 DR PIR; A02148; G2HU.
 DR HSSP; P01857; 1FC1.
 DR MIM; 147110; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
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 Query Match 38.5%; Score 475; DB 1; Length 326;
 Best Local Similarity 89.3%; Pred. No. 7e-34;
 Matches 92; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 125 ASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPPEVTVSWNSGALTSQVHTFFAVLOSS 184
 Db 1 ASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPPEVTVSWNSGALTSQVHTFFAVLOSS 60
 QY 185 GLYSLSSVTVPPSSSLGTQYICNVNHKPSNTKYDKKVEPKSC 227
 Db 61 GLYSLSSVTVPPSSSLGTQYTCNVHDKPSNTKYDKTVKRCCK 103
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-4 chain C region.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83157104; PubMed=6299662;
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE=70207560; PubMed=4192699;
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 constant region of a gamma 4 chain.";
 RL Biochem. J. 117:33-47(1970).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K01316; AAB59394.1; ALT_INIT.
 DR PIR; A02150; G4HU.
 DR HSSP; P01842; 7FAB.

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DR MIM; 147130; --
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN) .
FT DISULFID 27 83 INTERCHAIN (WITH A LIGHT CHAIN) .
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN) .
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN) .
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EP208E7A CRC64;

Query Match 38.4%; Score 474; DB 1; Length 327;
Best Local Similarity 91.1%; Pred. No. 8.6e-34;
Matches 92; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 125 ASTKGPSVFPLAASSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 184
Db 1 ASTKGPSVFPLAASCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60

Qy 185 GLYSLSSVTVTPSSSLGTQTYTCNVNHPKSNTKVDKKEPK 225
Db 61 GLYSLSSVTVTPSSSLGTQTYTCNVDPKPSNTKYDKRVESK 101

RESULT 4
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 33.7%; Score 416; DB 1; Length 120;
Best Local Similarity 60.5%; Pred. No. 2.6e-29;
Matches 75; Conservative 22; Mismatches 23; Indels 4; Gaps 2;
```

```
Qy 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETTHMWRQAPGKGLWVAGINPKNGGTS 60
Db 1 QVQLQPGTELKPKGASVNLSCASGYTFETSYMMHWIRQRPQGLEWIGGINPSNGGTY 60

Qy 61 NQRFMDRFTISVDKSTSTAYMQMNSLRADETAVYYCARWRGLNYGDFVRYFDVWGQGLV 120
Db 61 NQRFMDRFTISVDKSTSTAYMQMNSLRADETAVYYCARWRGLNYGDFVRYFDVWGQGLV 120

Qy 121 TVSS 124
Db 117 TVSS 120

RESULT 5
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -I- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match 32.9%; Score 405.5; DB 1; Length 117;
Best Local Similarity 61.3%; Pred. No. 2e-28;
Matches 76; Conservative 21; Mismatches 20; Indels 7; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETTHMWRQAPGKGLWVAGINPKNGGTS 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFETDYMKWQKSHGKSLWIGDINPNNGGTSY 60

Qy 61 NQRFMDRFTISVDKSTSTAYMQMNSLRADETAVYYCARWRGLNYGDFVRYFDVWGQGLV 120
Db 61 NQRFMDRFTISVDKSTSTAYMQMNSLRADETAVYYCARWRGLNYGDFVRYFDVWGQGLV 120

Qy 121 TVSS 124
Db 114 TVSS 117

RESULT 6
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
```

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 32.9%; Score 405.5; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 2e-28;
Matches 76; Conservative 19; Mismatches 19; Indels 13; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPGKLEWVAGINPKNGTSH 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFDTYMKWKVQSHGKSLIEWIGDINPNNGTST 60
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRADTAAYVCAR---WRGLNYGFDVRYFDVWGOG 117
Db 61 NQKFKGKATLVDKSSSPAYQLNSLTSEDSAVYYCARDRYW-----YFDVWGAG 110
QY 118 TLTVSS 124
Db 111 TTVTVSS 117

RESULT 7
HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT NON_TER 122 122
PYRROLIDONE CARBOXYLIC ACID.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 32.9%; Score 405.5; DB 1; Length 117;
Best Local Similarity 59.8%; Pred. No. 2e-28;
Matches 76; Conservative 19; Mismatches 19; Indels 13; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPGKLEWVAGINPKNGTSH 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYTFDTYMKWKVQSHGKSLIEWIGDINPNNGTST 60
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRADTAAYVCAR---WRGLNYGFDVRYFDVWGOG 117
Db 61 NQKFKGKATLVDKSSSPAYQLNSLTSEDSAVYYCARDRYW-----YFDVWGAG 110
QY 118 TLTVSS 124
Db 111 TTVTVSS 117

RESULT 7
HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A
CC PATIENT WITH MACROGLOBULINEMIA.
DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT NON_TER 122 122
PYRROLIDONE CARBOXYLIC ACID.
```

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SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 32.4%; Score 399; DB 1; Length 122;
Best Local Similarity 64.5%; Pred. No. 7.8e-28;
Matches 80; Conservative 13; Mismatches 29; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPGKLEWVAGINPKNGTSH 60
Db 1 QVELVESGGGVZPGRSLRUSCAASGFTFSNYAMHWVRQPPGKLEWVAVISYBGBKYY 60
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRADTAAYVCARWGLNYGFDVRYFDVWGOGTFLV 120
Db 61 ABSVKGFTISRDSEKETLYQMNSLRADTAAYVCARDREL-YG-BYRAFNWVGOGTFLV 118
QY 121 TVSS 124
Db 119 TVSS 122

RESULT 8
HV5I_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 104
FT DOMAIN 105 118
FT DISULFID 22 96
FT NON_TER 118 118
BY SIMILARITY.
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 32.0%; Score 395; DB 1; Length 118;
Best Local Similarity 58.9%; Pred. No. 1.7e-27;
Matches 73; Conservative 22; Mismatches 23; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPGKLEWVAGINPKNGTSH 60
Db 1 EVQLQQSGPELVKPGASVKISCRASGYTFDTYNNWVKQSHGKSLIEWIGDINPNNGTST 60
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRADTAAYVCARWGLNYGFDVRYFDVWGOGTFLV 120
Db 61 NQKFKGKATLVDKSSATYMLRSLTSEDSAVYYCAR---GYGDP--FDVWGOGTFTV 114
QY 121 TVSS 124
Db 115 TVSS 118

RESULT 9
HV1I_MOUSE STANDARD; PRT; 137 AA.
ID HV1I_MOUSE
```


OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81054880; PubMed=6776528;
RA Robinson E.A., Appella E.;
RT "Complete amino acid sequence of a mouse immunoglobulin alpha chain
(MOPC 511).";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMST5.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 31.7%; Score 391; DB 1; Length 122;
Best Local Similarity 61.1%; Pred. No. 3.8e-27;
Matches 77; Conservative 16; Mismatches 27; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYTFTYTHMWRQAPGKLEWVAGINPKNG--T 58
Db 1 EVKLVSGLVQPGGSLRLSCATGYTFTYTHMWRQAPGKLEWVAGINPKNG--T 60
QY 59 SHNQRFMDRTISVDKSTAYMQMNSILRAEDTAVYCARWGLNYGDFYFDVWGQGT 118
Db 61 EYSASVKGRTFIVSRDTSQILYLQMNALRAEDTAIYCAR--YFDVWGAGT 116
QY 119 LVTVSS 124
Db 117 TTVVSS 122

RESULT 12
HV20_MOUSE
ID HV20_MOUSE STANDARD; PRT; 122 AA.
AC P01789;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M603.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [2]
RP SEQUENCE OF 1-120.
RX MEDLINE=75017346; PubMed=4213527;
RA Rudikoff S., Potter M.;
RT "Variable region sequence of the heavy chain from a phosphorylcholine
binding myeloma protein.";
RL Biochemistry 13:4033-4038(1974).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE=75065510; PubMed=4530984;
RA Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Potter M.,
RA Davies D.R.;
RT "The three-dimensional structure of a phosphorylcholine-binding mouse

RT immunoglobulin Fab and the nature of the antigen binding site.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:4298-4302(1974).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR: A02070; AVMST5.
DR PDB: 1MCP; 15-JUL-92.
DR PDB: 2MCP; 15-JUL-92.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT SITE 33 33
H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
PHORYLCHOLINE.
FT SITE 52 52
H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
PHORYLCHOLINE.
FT STRAND 3 7
FT TURN 11 12
FT TURN 14 15
FT STRAND 17 25
FT HELIX 29 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 50
FT TURN 54 55
FT STRAND 61 61
FT TURN 64 66
FT STRAND 67 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 76 79
FT STRAND 80 86
FT HELIX 90 92
FT STRAND 94 103
FT STRAND 107 112
FT STRAND 116 120
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13626 MW; BA2C864438B64F0F CRC64;

Query Match 31.1%; Score 384; DB 1; Length 122;
Best Local Similarity 61.1%; Pred. No. 1.5e-26;
Matches 77; Conservative 13; Mismatches 30; Indels 6; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCATGYTFTYTHMWRQAPGKLEWVAGINPKNG--GT 58
Db 1 EVKLVSGLVQPGGSLRLSCATGYTFTYTHMWRQAPGKLEWVAGINPKNG--GT 60
QY 59 SHNQRFMDRTISVDKSTAYMQMNSILRAEDTAVYCARWGLNYGDFYFDVWGQGT 118
Db 61 EYSASVKGRTFIVSRDTSQILYLQMNALRAEDTAIYCAR--YFDVWGAGT 116
QY 119 LVTVSS 124
Db 117 TTVVSS 122

RESULT 13
HV38_MOUSE
ID HV38_MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;

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RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR; A02078; AVMST6.
DR HSSP; P01810; 2FB7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
KW NON_TER 119
FT SEQUENCE 119 AA; 13169 MW; BC38CC84E5EA00E8 CRC64;

Query Match 31.0%; Score 382; DB 1; Length 119;
Best Local Similarity 58.9%; Pred. No. 2.2e-26;
Matches 73; Conservative 18; Mismatches 27; Indels 6; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCAASGFTFTYTHMWRQAPGKGLEWVAGINPKNGTSH 60
DB 1 EVKLLEGGGLVQPGGSLRLSCAASGFTSRYWMSVWRQAPGKLEWIGEINPDSSTINY 60

QY 61 NQREMDRETISVDKSTSTAYMQMNSLRAEDTAVYICARWRGLNGYFDVYFDVWGOGTLV 120
DB 1 TPLSKDKFIISDNKNTLYLQMSKVRSEDYALYCAR---LCY---YGFYDWGAGTTFV 114

QY 121 TVSS 124
DB 115 TVSS 118

RESULT 14
HV3D_HUMAN
ID HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.-Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
DR PIR; A02048; H3HUTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
KW NON_TER 115
FT SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 30.9%; Score 380.5; DB 1; Length 115;
Best Local Similarity 62.1%; Pred. No. 2.9e-26;
Matches 77; Conservative 12; Mismatches 26; Indels 9; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFTEYTHMWRQAPGKGLEWVAGINPKNGTSH 60
```

```
DB 1 EVOLLESGGLVQPGGSLRLSCAASGFTFTYVMSWRQAPGKLZWWGAIZGLSVSZSY 60
QY 61 NQREMDRETISVDKSTSTAYMQMNSLRAEDTAVYICARWRGLNGYFDVYFDVWGOGTLV 120
DB 61 ABSVKGRTISDRDSSKNT----MNSLRAEDTAVYICARGKVSAY-----YFYGWZGTLV 111
QY 121 TVSS 124
DB 112 TVSS 115

RESULT 15
HV18_MOUSE
ID HV18_MOUSE STANDARD; PRT; 123 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (TEPC 15).
RX MEDLINE=76222762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
RN [2]
RP SEQUENCE FROM N.A. (H107).
RX MEDLINE=80199926; PubMed=6769593;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH.";
RL Cell 19:981-992(1980).
RN [3]
RP SEQUENCE (S107).
RX MEDLINE=76110488; PubMed=813561;
RA Rudikoff S., Barstad P., Potter M., Hood L.;
RL Unpublished results, cited by:
RL Hood L., Campbell J.H., Elgin S.C.R.;
RL Annu. Rev. Genet. 9:305-353(1975).
RN [4]
RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
RT "Ig antibodies to phosphorylcholine exhibit more diversity than
RT their Igm counterparts.";
RL Nature 291:29-34(1981).
CC -!- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
CC -!- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMST5.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123
FT SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 30.9%; Score 380.5; DB 1; Length 123;
Best Local Similarity 61.1%; Pred. No. 3.1e-26;
Matches 77; Conservative 13; Mismatches 31; Indels 5; Gaps 2;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFTEYTHMWRQAPGKGLEWVAGINPKNGS--T 58
DB 1 EVKLVEGGGLVQPGGSLRLSCATSGFTSDFYMEWYRQPPGKLEWIAASRNKANDYTT 60
```



```
QY 59 SHNOREMDREFTISVDKSTSTAYMOMNSIRAEDTAVYYCARWRGLNYGFDVRYFDYWGOGT 118
Db 61 EYSASVKGREFIVSRDTSQSILYLONNALRAEDTAIYYCAR---DYYGSSYWFYDWGAGT 117
QY 119 LTVVSS 124
Db 118 TTVVSS 123
```

Search completed: August 14, 2002, 11:07:34
Job time: 379 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:00:50 ; Search time 46.4 Seconds
(without alignments) 864.975 Million cell updates

```

Title: US-09-811-384-10
Perfect score: 1233
Sequence: 1 EQVLVESGGGLVQPGGSLRL.....PSNTKVDKKVEPKSCKDTH 232

```

Scoring table: BLOSUM62

Searched: 562222 seqs, 172994929

Total number of hits satisfying chosen parameter:

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45
```

Database : SPTREMBL_19:*

```

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_ordanelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	743.5	60.3	278	11	Q921K1	mus musculus
2	717.5	58.2	473	11	Q99125	mus musculus
3	709	57.5	473	11	Q99125	mus musculus
4	693	56.2	473	11	Q99125	mus musculus
5	682.5	55.3	468	11	Q99131	mus musculus
6	679.5	55.1	463	11	Q991C4	mus musculus
7	653.5	53.0	437	11	Q91A4	mus musculus
8	543	44.0	537	4	Q96BB9	homo sapien
9	508	41.2	494	4	Q96K68	homo sapien
10	501	40.6	614	4	Q96GA6	homo sapien
11	496.5	40.3	479	11	Q91WP5	mus musculus
12	489	39.7	488	11	Q91WR1	mus musculus
13	478.5	38.8	487	11	Q99KA4	mus musculus
14	477	38.7	486	11	Q91Z07	mus musculus
15	477	38.7	500	4	Q9BRV0	homo sapien
16	464	37.6	147	4	Q9Y509	homo sapien

17	464	37.6	484	11	Q99LA6	Q99LA6	mus	musculus
18	462.5	37.5	481	11	Q91WT1	Q91wt1	mus	musculus
19	456.5	37.0	480	11	Q91XE1	Q91xe1	mus	musculus
20	455	36.9	496	4	Q96DK0	Q96dk0	homo	sapient
21	445.5	36.1	481	11	Q91WT3	Q91wt3	mus	musculus
22	431	35.0	143	11	Q924Q5	Q924q5	mus	musculus
23	427.5	34.7	142	11	Q924Q1	Q924q1	mus	musculus
24	427.5	34.7	146	11	Q924R8	Q924r8	mus	musculus
25	425.5	34.5	144	11	Q924P5	Q924p5	mus	musculus
26	424	34.4	597	4	Q9BU10	Q9bu10	homo	sapient
27	424	34.4	618	4	Q96AA6	Q96aa6	homo	sapient
28	420	34.1	597	4	Q9BQB8	Q9bqb8	homo	sapient
29	419	34.0	145	11	Q924Q7	Q924q7	mus	musculus
30	418	33.9	143	11	Q924R0	Q924r0	mus	musculus
31	418	33.9	145	11	Q924R3	Q924r3	mus	musculus
32	415	33.7	137	11	Q924R6	Q924r6	mus	musculus
33	415	33.7	143	11	Q924R7	Q924r7	mus	musculus
34	414	33.6	145	11	Q924R1	Q924r1	mus	musculus
35	412	33.4	145	11	Q924R4	Q924r4	mus	musculus
36	410	33.3	143	11	Q91VA2	Q91va2	mus	musculus
37	409.5	33.2	140	11	Q924P8	Q924p8	mus	musculus
38	409	33.2	145	11	Q924P7	Q924p7	mus	musculus
39	406.5	33.0	146	11	Q924Q3	Q924q3	mus	musculus
40	404.5	32.8	613	4	Q96EY0	Q96ey0	homo	sapient
41	404	32.8	145	11	Q924Q9	Q924q9	mus	musculus
42	404	32.8	145	11	Q924Q6	Q924q6	mus	musculus
43	404	32.8	482	11	Q91X92	Q91x92	mus	musculus
44	403.5	32.7	140	11	Q924R2	Q924r2	mus	musculus
45	401.5	32.6	113	4	Q9UL90	Q9ul90	homo	sapient

ALIGNMENTS

RESULT	I
Q921KI1	
ID	Q921K1
PRT:	PRELIMINARY;
AA:	278 AA.
AC	A921K1;
DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	UNKNOWN PROTEIN FOR MGC:18977).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Straussberg R.;
RL	Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC012207; AAH12207.1; --
SO	SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 60.3%; Score 743.5; DB 11; Length 278;
Best Local Similarity 60.9%; Pred. No. 3.le-59;
Matches 137; Conservative 39; Mismatches 44; Indels 5; Gaps 2;

[illegible]


```
DR EMBL; BC010327; AAH0327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match      56.2%; Score 693; DB 11; Length 473;
Best Local Similarity 57.4%; Pred. No. 2.2e-54;
Matches 140; Conservative 30; Mismatches 50; Indels 24; Gaps 4;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 60
Db 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 60
QY 20 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 79
Db 20 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 79
QY 61 NQRFMDRFTISVDKSTAYMOMNSLRADTAAYYCAR--WRGLNYGDFVDFVWGQGT 118
Db 61 NQRFMDRFTISVDKSTAYMOMNSLRADTAAYYCAR--WRGLNYGDFVDFVWGQGT 118
QY 80 ADTVKGFTISRDAKNTFLQMTSLRSEDYAMYYCARELW-----LRRIDYWGQGT 131
Db 80 ADTVKGFTISRDAKNTFLQMTSLRSEDYAMYYCARELW-----LRRIDYWGQGT 131
QY 119 LVTVSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPP 178
Db 119 LVTVSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPP 178
QY 132 TIIVSSAKTPPSVYPLAPGCGDTGGSSVTGLGKVGYPESVTVWNSGSLSSSVHTFPP 191
Db 132 TIIVSSAKTPPSVYPLAPGCGDTGGSSVTGLGKVGYPESVTVWNSGSLSSSVHTFPP 191
QY 179 AVLOSGGLYSLSSVTVPSSTSGTQTYICNVNHNKPSNTKVDKKVEP-----K 225
Db 179 AVLOSGGLYSLSSVTVPSSTSGTQTYICNVNHNKPSNTKVDKKVEP-----K 225
QY 192 ALLO-SGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSGPSTINPCPPCK 250
Db 192 ALLO-SGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTTVDKKLEPSGPSTINPCPPCK 250
QY 226 SCDK 229
Db 226 SCDK 229
QY 251 ECHK 254
Db 251 ECHK 254

RESULT 5
QY99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match      55.3%; Score 682; DB 11; Length 468;
Best Local Similarity 57.3%; Pred. No. 2.1e-53;
Matches 129; Conservative 40; Mismatches 50; Indels 6; Gaps 3;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 60
Db 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 60
QY 20 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 79
Db 20 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 79
QY 61 NQRFMDRFTISVDKSTAYMOMNSLRADTAAYYCARWGLNYGDFVDFVWGQGT 120
Db 61 NQRFMDRFTISVDKSTAYMOMNSLRADTAAYYCARWGLNYGDFVDFVWGQGT 120
QY 80 APRQDKATITADTSSNTAYLQLSLTSEDYAIYYCA--RNLLYG---GYDYWGQGT 134
Db 80 APRQDKATITADTSSNTAYLQLSLTSEDYAIYYCA--RNLLYG---GYDYWGQGT 134

QY 121 TVSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
QY 135 TVSSAKTTPSPVYPLAPGCGDTGGSSVTGLGKVGYPESVTVWNSGSLSSSVHTFPAV 194
Db 135 TVSSAKTTPSPVYPLAPGCGDTGGSSVTGLGKVGYPESVTVWNSGSLSSSVHTFPAV 194
QY 181 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHNKPSNTKVDKKVEPK 225
Db 181 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHNKPSNTKVDKKVEPK 225
QY 195 LQSD-LYTLSSSVTVPSSTWPSQITCNVAHPASSTKVDKKIEPR 238
Db 195 LQSD-LYTLSSSVTVPSSTWPSQITCNVAHPASSTKVDKKIEPR 238

RESULT 6
QY99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match      55.1%; Score 679.5; DB 11; Length 463;
Best Local Similarity 57.7%; Pred. No. 3.6e-53;
Matches 131; Conservative 38; Mismatches 53; Indels 5; Gaps 3;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 60
Db 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWRQAPGKGLWVAGINPKNGTSH 60
QY 20 QVQLQSGAELRPGASVRLSCKASGYTFGTGYGSWVKQRTGGQGLEWVGEIYPCSGNTY 79
Db 20 QVQLQSGAELRPGASVRLSCKASGYTFGTGYGSWVKQRTGGQGLEWVGEIYPCSGNTY 79
QY 61 NQRFMDRFTISVDKSTAYMOMNSLRADTAAYYCARWGLNYGDFVDFVWGQGT 120
Db 61 NQRFMDRFTISVDKSTAYMOMNSLRADTAAYYCARWGLNYGDFVDFVWGQGT 120
QY 80 SEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAVYFCA--RSSYYSYDL--FAYWGQGT 135
Db 80 SEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAVYFCA--RSSYYSYDL--FAYWGQGT 135
QY 121 TVSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
QY 136 TVSAKTTPSPVYPLAPGSAQTNSMVTGLGKVGYPESVTVWNSGSLSSSVHTFPAV 195
Db 136 TVSAKTTPSPVYPLAPGSAQTNSMVTGLGKVGYPESVTVWNSGSLSSSVHTFPAV 195
QY 181 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
Db 181 LQSSGLYSLSSVTVPSSTSGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
QY 196 LQSD-LYTLSSSVTVPSSTWPSQITCNVAHPASSTKVDKKIYPRDC 241
Db 196 LQSD-LYTLSSSVTVPSSTWPSQITCNVAHPASSTKVDKKIYPRDC 241

RESULT 7
QY9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.:
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152372; AAD40243.1; -.
 DR HSP; p01842; 7FAB.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_4.
 DR SMART; SM00406; Igv; 1.
 DR SMART; SM00410; Ig_Like; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1
 FT 437 437
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

 Query Match 53.0%; Score 653.5; DB 11; Length 437;
 Best Local Similarity 58.4%; Pred. No. 7.3e-51;
 Matches 132; Conservative 26; Mismatches 57; Indels 11; Gaps 3;

 QY 2 VOLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLVWVAGINPKNGCTSHN 61
 Db 1 VOLVESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQTPERKLEWVASFS-SGGIIYYT 59

 QY 62 QRPMDFRTISVDKSTSTAYMQMNSLRAEDTAVYICARWRGLNYGDFVYFDVWGQGLT 121
 Db 60 DSVKGRFTIYKDKRNILSLQMSLSRSEDAMYCARG-----DYSAYWGPGTGLT 110

 QY 122 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHTEPPAVL 181
 Db 111 VSAAKTTPPSVYPLAPGSAAGTNSMTLGLCLVKGYFPEPTVTWNSGSLSSGVTTPAVL 170

 QY 182 QSSGLYSLSVVTPVPSLSLGTQYICNVNHKPSNTKVKDKKVEPKSC 227
 Db 171 QSD-LYLLSSSVTPSPSTWPSSETVTCNVAHPASSTKVKDKKIIPRDC 215

 RESULT 8
 Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC Q96BB9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHEICAL 65.0 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
 RA Strausberg R.:
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015760; AAH15760.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

 Query Match 44.0%; Score 543; DB 4; Length 597;
 Best Local Similarity 51.4%; Pred. No. 1e-40;
 Matches 114; Conservative 31; Mismatches 69; Indels 8; Gaps 6;

 QY 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLVWVAGINPKNGCTSH 60
 Db 20 EVOLLESGGGLVQPGGSLRLSCAASGFTSSYAMNVRQAPGKGLVWVSAISGSGSTYY 79

QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICAR-WRGLNYGDFVYFDVWGQGL 119
 Db 80 ADSVKGRFTISRDNSRDTLYLQMNLSLRAEDTAVYICAKDPRGYSAGSNYTRDYWGQGL 139

 QY 120 VTVSSASTKGPSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSVGH 176
 Db 140 VTVSSGASAPTLPLVLVSCENSPTSSTVAVGCLAQDPLPDSITFSWKYKNNSDISSTRG 199

 QY 177 FPAVLQSSGLYSLSVVTPVPSLSL--GTQTY-ICNVNHKPSN 215
 Db 200 FPSVLR-GGKYAATSOVLLPSKQDVWQGTDEHVCKVQHPNGN 240

 RESULT 9
 Q96K68 ID Q96K68 PRELIMINARY; PRT; 494 AA.
 AC Q96K68;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE CDNA FLJ14473 FTS. CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO
 DE SAPIENS SNC73 PROTEIN (SNC73) MRNA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY GLAND;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma T., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK027379; BAB5072.1; -.
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AEE4C0E CRC64;

 Query Match 41.2%; Score 508; DB 4; Length 494;
 Best Local Similarity 49.8%; Pred. No. 1.2e-37;
 Matches 108; Conservative 34; Mismatches 63; Indels 12; Gaps 6;

 QY 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLVWVAGINPKNGTSH 60
 Db 20 EVOLVESGGGLVQPGGSLRLSCAASGLSFSTYAMNVRQAPGKGLVWVSSISRSYTY 79

 QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYICARWR--GLNYGDFVYFDVWGQ 117
 Db 80 RDSVKGRFTISRDNAKNSLYLQMNLSLRVDDTAVYICARDSGCAICYG-----FSPWGQ 134

 QY 118 TLTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFP-EPVTVSWNSGALTSVGH 176
 Db 135 TLTVSSASTSPKVPFLSLCS-TQPDGNVVIACLVGFFPQEPPLSVTWSGSGGVYARN 193

 QY 177 FPAVLQSSG-LYSLSSVVTPVPSLS-LGTQTYICNVNH 211
 Db 194 FPPSQDASGDLYTSSQLTPATQCLAGKSVTCHKV 230

 RESULT 10
 Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
 AC Q96GA6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE UNKNOWN (PROTEIN FOR MGC:15420).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strassberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.l; -.
SQ SEQUENCE 614 AA; 67921 MW; 55FEF36E77AA9BBB CRC64;

Query Match 40.6%; Score 501; DB 4; Length 614;
Best Local Similarity 45.7%; Pred. No. 6.6e-37;
Matches 101; Conservative 45; Mismatches 65; Indels 10; Gaps 7;

Qy	1	EVQLVESGGGLVPGGSLRLSQCATSYTFTEYTHMMWRAPAGKLEWVAGLNPKNCGTSH	60
Db	20	QMLVQSGASGVKKTGSSVKSCASGYTFRYRLHWVRAPQGALEWGMGWIPTFNGNTNY	79
Qy	61	NOREMDREFTISVDKSNSTAYKMNLSRAEDTAYYYCARWRLNGYFDVRYEDVWGCGTLV	120
Db	80	AQKFQDRVITIRDSMNTAYEULSSKSEDTAMYYCA--RGYSSSWD--DAFDLWGCGTWY	136
Qy	121	TVSASATKGPSVPEPLAPSSKSTSG-GTAALGLGLVKDYFPEPTVSW--NSGALTSGVHTF	177
Db	137	TVSSGSASATPLPFLYSCENSPDTSVAVGCLAQDFLDSITFSWKYKNSDISSTRGF	196
Qy	178	PAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHPKSN	215
Db	197	PSVLR--GGKTAATSQVLLPSQVMQVGGTDEHVCKVQHPNGN	236

```

RESULT 11
Q91WP5 PRELIMINARY; PRT; 479 AA.
ID Q91WP5
AC Q91WP5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DE HYPOTHETICAL 51.6 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=COLON;
RC
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC013656; AAH13656.1; -.
KW Hypothetical protein.
SQ SEQUENCE 479 AA; 51603 MW; ECBD0877748584F CRC64;

```

Query Match	40.38;	Score	496.5;	DB	11;	Length	479;
Best Local Similarity	44.4;	Pred. No.	1.2e-36;				
Matches	107;	Conservative	31;	Mismatches	78;	Indels	25;
Gaps							

QY	1	EVQLVESGGGLVPGGSLRLSCA	SYGTFTEYTHWMRQAPKGL	EWAGINPKNGG	TS	60
Db	20	EVQLVESGGGLVPGGSLKVC	ASGLTFSNYMSWVRQSP	KEKRL	EWAAINSGNG	79
QY	61	NOREMDRFTISVDKSTSTAY	WOMNSLR	EDTA	VYCCARWGLN	120
Db	80	SDTMKGRFTISRDNAKST	LYLQMSLS	EDTA	FYCYVRG	130
QY	121	TVSSASTKGPSVFPLA	PSKSTSGT	ALGCLV	KDYD	179
Db	131	TVSSEAPREPIYPLT	-FPQALSD	DPVI	IGCLIH	189
QY	180	VLOQSGGLYSLSVSWY	FSSSLGT-Q	TVICN	VNHRPS	226

```

Db      190  ALASGRRTMSSQLTLPAVECPGESVKCSVQH-DSNPVQELNVNCPGICSPPTPTPPPPS 248
Qy      227  C 227
        |
Db      249  C 249

RESULT 12
Q91WR1
ID      Q91WR1      PRELIMINARY;      PRT;      488 AA.
AC      Q91WR1;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      DE HYPOTHETICAL 53.0 KDA PROTEIN.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
[1]
RN      SEQUENCE FROM N.A.
RP      TISSUE=KIDNEY;
RC      R.
RA      Strausberg R.;
RL      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC013539; AAH13539.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

```

Query Match 39.7%; Score 489; DB 11; Length 488;
Best Local Similarity 42.3%; Pred. No. 6e-36;

Qy	1	EVQLVESGGGLVPGGSLRLSCATSGYTFTEYTHMHMRQAPGKGLEWVAGINPKNGTSH	60
		: : : : : : : : : : : : : : : :	
Db	20	EVQLQQSGPELVKPGASVKLSCKASGITIDYVYNNVKQSHGSKSLEWIGDINPYNGTSTY	79
		: : : : : : : : : : : : : : : :	
Qy	61	NOREMDRFETISVDKSTSTAYMOMNSLRADPAVYICARWGLNYPGVRYFDVWGQGTLY	120
		: : : : : : : : : : : : : : : :	
Db	80	NQKFKGKATLVDKSSLIAYMQLNNLISDQASVYICARGPVYISYFYSDRGDVTWGQGTLY	139
		: : : : : : : : : : : : : : : :	
Qy	121	TVSSASTKGPSVFFLAPSSKSTSGGTAAALGCLVKDYDE- PVTVSMNSGALTSGVHTFPA	179
		: : : : : : : : : : : : : : : :	
Db	140	TVSAPAPAREPTIYPLT-FPQALSSDPVVIIGLIHDYFPGSGTMNVTGWKSGKDITTVNFP	198
		: : : : : : : : : : : : : : : :	
Qy	180	VLQSSGGLYSLSVVTVFPSSSLGT- QTVICNNHNPSTKVDKKVE-----PKS	236
		: : : : : : : : : : : : : : : :	
Db	199	ALASGGRYTMSQTLTFAVECPGESVKCSVQH-DSNPVOELNNVNCPCIGICSPPTTPPPPS	257
		: : : : : : : : : : : : : : : :	
Qy	227	C	227
Db	258	C	258

RESULT		13	
ID	Q99KA4		PRELIMINARY; PRT;
AC	Q99KA4:		
DT	01-JUN-2001	(TrEMBLrel.	17,
DT	01-JUN-2001	(TrEMBLrel.	17,
DT	01-DEC-2001	(TrEMBLrel.	19,
DE	HYPOTHETICAL 52.6 KDA PROTEIN.		
OS	Mus musculus	(Mouse).	
OC	Eukaryota;	Metazoa;	Chordata;
OX	Mammalia;	Eutheria;	Rodentia;
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Straussberg R.;		
RL	Submitted (MAR-2001)		
DR	EMBL; BC004786; AAH04786.1;	- ,	
DR	HSSP; P01810; 2FBJ.		
DR	InterPro; IPR003599; Iq.		

```
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 38.8%; Score 478.5; DB 11; Length 487;
Best Local Similarity 44.4%; Pred. No. 5.3e-35;
Matches 107; Conservative 35; Mismatches 82; Indels 17; Gaps 8;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPKGLEWVAGINPKNGGTS 60
DB 20 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPKGLEWVAGINPKNGGTS 60
QY 61 NQRFMDRTISVDKSTAYMQMNSLRADTAAYVCAR-WRGLNYCFDVRVFDVWGQGL 119
DB 80 PDNVKGRFTISRDNKAKNLYLQMSHLKSEDTAMYYKCDMGSPGYGYSR-FDYWGQGT 138
QY 120 VTSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGVHTFP 178
DB 139 ITVSSESARNPTIYPLT-LPRALSSDPVIIGLIHDYFPGTMNVTWGSKGDIITVNPFP 197
QY 179 AVLOSSGLYSLSSVVPSSSLGT-QTYICNVNHRKPSNT--KVDKKVE-----PKS 226
DB 198 PALASGGGYTWSSQLTLPAVECPGESVKCSYQH-DSNAVQELDVKCSGPPPPCPPPS 256
QY 227 C 227
DB 257 C 257

RESULT 14
Q91207 PRELIMINARY; PRT; 486 AA.
AC Q91207;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 52.7 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

Query Match 38.7%; Score 477; DB 11; Length 486;
Best Local Similarity 42.9%; Pred. No. 7.2e-35;
Matches 103; Conservative 36; Mismatches 85; Indels 16; Gaps 7;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPKGLEWVAGINPKNGGTS 60
DB 20 EVHLVESGGGLVQPGGSLRLSCVSGSFTSYDMSWVRQTPERRLEWVAAIT-SGGNTYY 78
QY 61 NQRFMDRTISVDKSTAYMQMNSLRADTAAYVCARWGLNYCFDVRVFDVWGQGLV 120
DB 129 PDNVKGRFTISRDNKAKNLYLQMSHLKSEDTAMYYCVPRPEIYYISGYFDSWGQGTI 138
QY 121 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGVHTFPA 179
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DB 139 TVSSSESARNPTIYPLT-LPRALSSDPVIIGLIHDYFPGTMNVTWGSKGDIITVNPFP 197
QY 180 VLOSSGLYSLSSVVPSSSLGT-QTYICNVNHRKPSNT--KVDKKVE-----PKSC 227
DB 198 ALASGGGYTWSSQLTLPAVECPGESVKCSYQH-DSNAVQELDVKCSGPPPPCPPPSC 256

RESULT 15
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE HYPOTHETICAL 54.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; Igcl; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 38.7%; Score 477; DB 4; Length 500;
Best Local Similarity 44.7%; Pred. No. 7.5e-35;
Matches 98; Conservative 42; Mismatches 69; Indels 10; Gaps 6;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWRAQPKGLEWVAGINPKNGGTS 60
DB 20 QVHLVSGAEVMSGASRVVSKTSGYAFHTYIIWVRQAPGQGLEWGWISPSDNTRF 79
QY 61 NQRFMDRTISVDKSTAYMQMNSLRADTAAYVCARWGLNYG-----FDVRYFDVWG 115
DB 80 AKKFGQRTVLTDTSTSTVYMELSRLSRDDTAAYVCAR-RYCSYSSQNDYIIYMDVWG 138
QY 116 QGTLTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPE-PVTVSWNSGALTSGV 174
DB 139 KGTTVTVSSASPTSPKVFPLSLCS-TQPDGNVIACLVQGFQEPPLSVTSSESQGVTA 197
QY 175 HTPFAVLQSSG-LYSLSSVVPSSS-LGTQTYICNVNH 211
DB 198 RNPPSODASGDLTYTSSQLTLPATQCLAGKSVTCHVKH 236

Search completed: August 14, 2002, 11:07:12
Job time: 382 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:51:59 ; Search time 54.11 Seconds
(without alignments)
476.236 Million cell updates/sec

Title: US-09-811-384-10

Perfect score: 1233

Sequence: 1 EVOLVESGGLVPGGSLRL.....PSNFKVDKVPKSCDKTHT 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1233	100.0	232	18 AAW34503	Heavy chain of hum
2	1233	100.0	232	20 AAY08753	Human antibody huH
3	1233	100.0	241	20 AAW95614	Humanized anti-CD1
4	1233	100.0	241	22 AAB66776	rhuMAB CD18 heavy
5	1233	100.0	277	20 AAW30631	Recombinant humani
6	1233	100.0	300	20 AAW95623	PS1130 expression
7	1233	100.0	300	22 AAW30635	Recombinant humani
8	1233	100.0	300	22 AAB66785	Protein encoded by
9	1233	100.0	537	21 AAB03664	Anti-CD18 antibody
10	1137	92.2	450	18 AAW34505	Heavy chain of ful
11	1137	92.2	450	20 AAY08755	Human IgG2 huH52 h

12	1116	90.5	552	14	AAW30775	pH52-8.0 humanised
13	1094	88.7	232	17	AAW00374	Anti-CD18 chimeric
14	1091	88.5	454	14	AAW30774	H52H4-160 murine a
15	1030	83.5	253	20	AAW29444	Humanised anti-IL-
16	1030	83.5	253	20	AAW29444	Humanised anti-IL-
17	1030	83.5	253	21	AAW30314	Humanised anti-IL-
18	1030	83.5	253	21	AAW30316	6G4-2-5V11 heavy c
19	1030	83.5	253	21	AAW77757	Humanised anti-IL-
20	1030	83.5	253	21	AAW77759	Humanised anti-IL-
21	1030	83.5	256	19	AAW69304	Humanised anti-IL-
22	1030	83.5	256	20	AAW29457	6G4V11N35A Fab' he
23	1030	83.5	256	21	AAW30321	Humanised anti-IL-
24	1030	83.5	256	21	AAW77765	Humanised anti-IL-
25	1030	83.5	298	19	AAW69303	Humanised anti-IL-
26	1030	83.5	298	20	AAW29456	Humanised anti-IL-
27	1030	83.5	298	21	AAW30319	Humanised anti-IL-
28	1030	83.5	298	21	AAW77762	Anti-IL-8 6G4-2-5V
29	1030	83.5	452	20	AAW29458	Humanised anti-IL-
30	1030	83.5	452	21	AAW30322	Recombinant immuno
31	1030	83.5	452	21	AAW77766	Humanised anti-IL-
32	1021	82.8	452	19	AAW69316	Anti-IL-8 humanise
33	1007.5	81.7	412	19	AAW70672	Protein encoded by
34	989	80.2	461	13	AAW24048	Heavy chain of 4D5
35	989	80.2	527	22	AAW82925	Anti-HER2 HuMab4D5
36	989	80.2	698	20	AAW83493	4D5 Fab molecule e
37	980.5	79.5	449	21	AAW68810	A rat heavy chain
38	966.5	78.4	229	20	AAW95665	Mus musculus anti-
39	966.5	78.4	229	22	AAW76954	Variable heavy cha
40	966.5	78.4	233	20	AAW95670	Mus musculus anti-
41	966.5	78.4	233	22	AAW76959	Variable heavy cha
42	966.5	78.4	451	20	AAW95659	Mus musculus anti-
43	966.5	78.4	451	20	AAW95661	Mus musculus anti-
44	966.5	78.4	451	21	AAW5201	Light chain amino
45	966.5	78.4	451	22	AAW47088	Anti-IgE antibody,

ALIGNMENTS

RESULT 1
AAW34503
ID AAW34503 standard; protein; 232 AA.
XX
AC AAW34503;
XX
DT 19-MAR-1998 (first entry)
XX
DE Heavy chain of humanised H52 antibody.
XX
KW Humanised antibody; HUH52; heavy chain; focal ischaemic stroke; embolism;
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;
KW systemic hypoperfusion; cardiac arrest.
XX
OS Synthetic.
OS Homo sapiens.
OS Mus sp.
XX
PN WO926912-A2.
XX
PD 31-JUL-1997.
XX
PF 11-JAN-1997; 97WO-US00492.
XX
PR 23-JAN-1996; 96US-0589982.
XX
PA (GETH) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
PI Bednar MM, Gross CE, Thomas GR;
XX WPI; 1997-393373/36.
XX

PT Administering an anti-CD18 antibody to treat focal ischaemic stroke
 PT - by increasing cerebral blood flow and reducing size of brain
 PT infarct
 XX
 XX
 PS
 PS
 XX Disclosure; Page 9; 41pp; English.
 CC
 CC This sequence represents the heavy chain of the humanised H52 antibody.
 CC The H52 antibody can be used in the method of the invention. The method
 CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
 CC interrupted blood supply, in a mammal, caused by obstruction of a main
 CC cerebral artery, comprises administering anti-CD18 antibody to increase
 CC cerebral blood flow and/or reduce the size of the area of brain that
 CC dies, without removing the arterial obstruction. CD18, is upregulated in
 CC patients after ischaemic stroke or transient ischaemic attack (stroke
 CC symptoms last less than 24 hours with complete recovery). Treatment with
 CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
 CC infarct size, improving clinical outcomes in focal ischaemic strokes in
 CC mammals, particularly in humans. The method provides an alternative to
 CC thrombolytic therapy for treating ischaemic strokes caused by
 CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
 CC therapy has been unsuccessful, is contra-indicated e.g. because such
 CC drugs exacerbate bleeding, or is unsuitable because of the time delay
 CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
 CC plasminogen activator) may also be administered before, after or
 CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
 CC be used to treat the third main type of ischaemic stroke, systemic
 CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
 XX
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1233; DB 18; Length 232;
 Best Local Similarity 100.0%; Pred. No. 4.5e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETTHMWRQAPGKLEWVAGINPKNGTSH 60
 Db 1 evqlvesggglvqpqgsirlscatsgytfttymhmrqapgkglewvaginpkngtsh 60
 QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGDFVRYDVGQGTIV 120
 Db 61 nqrfmdrftisvdkstststaymqmnsdraedtavyycarwrglnygfdrfydvwgggtlv 120
 QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAY 180
 Db 121 tvssastkgpsvfplapsskstsggtaalgclvkdypfpptvswnsгалtsvhtfpay 180
 QY 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHT 232
 Db 181 lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232

RESULT 2
 AAY08753
 ID AAY08753 standard; protein; 232 AA.
 XX
 AC AAY08753;
 XX
 XX
 DT 10-AUG-1999 (first entry)
 XX
 XX Human antibody huH52 heavy chain protein fragment.

XX IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
 KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
 KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;
 KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
 KW antibody; huH52; heavy chain.
 XX
 XX Homo sapiens.
 OS
 XX
 XX *US5914112-A.
 PN
 XX
 XX 22-JUN-1999.
 PD

XX 22-JAN-1997; 97US-0788800.
 PF
 XX
 PR 23-JAN-1996; 96US-0093038.
 PR 22-JAN-1997; 97US-0788800.
 XX
 PA (SETH) GENENTECH INC.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX
 XX Bednar MM, Gross CE, Thomas GR;
 XX WPI; 1999-370483/31.
 DR
 XX
 PT Anti-CD18 antibodies in stroke
 XX
 PS Claim 11; Column 29-32; 25pp; English.
 CC
 CC This invention describes a method for improving the clinical outcome in
 CC focal ischaemic stroke by administering novel anti-CD18 antibody which
 CC has cerebroprotective properties. The invention particularly describes a
 CC method of treating focal ischaemic stroke caused by the obstruction of a
 CC main cerebral artery which comprises administering an anti-CD18 antibody
 CC to increase the blood flow or reduce the infarct size, where: (1) the
 CC antibody binds to an extracellular domain of CD18 and inhibits or reduces
 CC the ability of the cell expressing CD18 to bind to endothelium, (2) the
 CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the
 CC antibody dissociates CD11b/CD18 complex. This sequence represents the
 CC human antibody huH52 heavy chain region.
 XX
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1233; DB 20; Length 232;
 Best Local Similarity 100.0%; Pred. No. 4.5e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETTHMWRQAPGKLEWVAGINPKNGTSH 60
 Db 1 evqlvesggglvqpqgsirlscatsgytfttymhmrqapgkglewvaginpkngtsh 60
 QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGDFVRYDVGQGTIV 120
 Db 61 nqrfmdrftisvdkstststaymqmnsdraedtavyycarwrglnygfdrfydvwgggtlv 120
 QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAY 180
 Db 121 tvssastkgpsvfplapsskstsggtaalgclvkdypfpptvswnsгалtsvhtfpay 180
 QY 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHT 232
 Db 181 lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232

RESULT 3
 AAW95614
 ID AAW95614 standard; protein; 241 AA.
 XX
 AC AAW95614;
 XX
 XX 08-JUN-1999 (first entry)
 DT
 XX
 XX Humanized anti-CD18 antibody rhuMab CD18 heavy chain.
 DE
 XX
 KW Monoclonal antibody; heavy chain; humanized; myocardial infarction;
 KW burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;
 KW hemorrhagic; stroke.
 XX
 XX Mus musculus.
 OS
 OS Synthetic.
 XX
 XX WO9856418-A1.
 PN
 XX
 XX 17-DEC-1998.
 PD

XX PF 12-JUN-1998; 98WO-US12334.
 XX PR 13-JUN-1997; 97US-0050951.
 XX PA (GETH) GENENTECH INC.
 XX PI Blank GS, Narindray DS, Zapata GA;
 XX DR WPI; 1999-060267/05.
 XX PT New method for recovering polypeptides from cell cultures - by
 XX PT treating with reagent and filtering to remove reagent
 XX PS Example; Fig 1A; 43pp; English.
 XX CC A method has been developed for recovering a polypeptide comprising: (a)
 CC exposing a composition comprising a polypeptide to a reagent which binds
 CC to or modifies the polypeptide, where the reagent is immobilized on a
 CC solid phase; and (b) passing the composition through a filter bearing an
 CC opposite charge to the reagent so as to remove leached reagent from the
 CC composition. The present invention also describes a method for modifying
 CC a precursor antibody comprising a leucine zipper by exposing the
 CC precursor antibody to a protease immobilized on a solid support so that
 CC the protease removes the zipper. The methods can be used to purify
 CC proteins from cell cultures. They are especially useful for isolating
 CC antibodies. The methods overcome the problem of reagent leakage into the
 CC protein as is the case in prior art immobilized modification systems. By
 CC using a opposite charge filter the reagent can be excluded from the
 CC sample, preventing contamination. The present sequence represents the
 CC recombinant humanised anti-CD18 antibody (rhuMab CD18) heavy chain,
 CC which is used in an example from the present invention.
 XX SQ Sequence 277 AA;

Query Match 100.0%; Score 1233; DB 20; Length 277;
 Best Local Similarity 100.0%; Pred. No. 5.5e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGSLRLSCATSGYTFEYTHWMRQAPGKLEWVAGINPKNGGTS 60
 Db 1 evqlvesggglvqpqgslrlscatsgytfttymhmraqpdkglewaginpknngtsh 60
 QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLTV 120
 Db 61 nqrfmdrtisvdkststaymqmnsrlraedtavyycarwrglnygfdvryfdvvgggtlv 120
 QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
 Db 121 tvssastkgpsvfpplapssksts ggtaalgc lvkdyfpeptvswns galtsgvhtfpav 180
 QY 181 LQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKVPKSCDKTHT 232
 Db 181 lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkvpkscdktht 232

RESULT 6
 AAW95623
 ID AAW95623 standard; Protein; 300 AA.
 XX AC AAW95623;
 XX DT 08-JUN-1999 (first entry)
 XX DE pS1130 expression cassette encoded rhuMab CD18 heavy chain.
 XX KW Monoclonal antibody; heavy chain; humanized; myocardial infarction;
 XX KW burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;
 XX KW hemorrhagic; stroke; heavy chain.
 XX OS Mus musculus.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT sig_peptide 1..23
 XX PN WO9856418-A1.
 XX PD 17-DEC-1998.
 XX XX 12-JUN-1998; 98WO-US12209.
 XX PF 13-JUN-1997; 97US-0874897.
 XX PR (GETH) GENENTECH INC.
 XX PA
 XX PI Lam XM, Oeswein JQ, Ongpipattanakul B, Shahroksh Z;
 XX PI Wang SX, Weissburg RP, Wong RL;
 XX DR WPI; 1999-080860/07.
 XX PT New stable aqueous antibody formulations - comprising an antibody
 XX PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5
 XX PT - 6, a surfactant and a polyol
 XX PS Disclosure; Fig 21A; 87pp; English.
 XX CC The sequence is that of the pS1130 encoded heavy chain of a humanized
 CC murine anti-CD18 antibody rhuMab CD18. It can be used for the treatment
 CC of disorders which include haemorrhagic shock, thermal injury (such
 CC as that resulting from burns), stroke (including ischaemic and
 CC haemorrhagic stroke) and myocardial infarction. The antibody
 CC formulation can be stabilised at a temperature of 2-8 deg. C
 CC for at least one year or at a temperature of 30 deg. C for at
 CC least one month and is stable following freezing and thawing.
 XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1233; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 6.1e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGSLRLSCATSGYTFEYTHWMRQAPGKLEWVAGINPKNGGTS 60
 Db 24 evqlvesggglvqpqgslrlscatsgytfttymhmraqpdkglewaginpknngtsh 83
 QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLTV 120
 Db 84 nqrfmdrtisvdkststaymqmnsrlraedtavyycarwrglnygfdvryfdvvgggtlv 143
 QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
 Db 144 tvssastkgpsvfpplapssksts ggtaalgc lvkdyfpeptvswns galtsgvhtfpav 203
 QY 181 LQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKPSNTKVDKVPKSCDKTHT 232
 Db 204 lqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkvpkscdktht 255

RESULT 7
 AAW30635
 ID AAW30635 standard; protein; 300 AA.
 XX AC AAW30635;
 XX DT 06-APR-1999 (first entry)
 XX DE Recombinant humanised anti-CD18 antibody rhuMab CD18 heavy chain.
 XX KW Recombinant humanised anti-CD18 antibody; rhuMab CD18; leucine zipper;
 XX KW murine monoclonal antibody; muMab #52; protein recovery; filtration;
 XX KW chromatography.
 XX OS Mus sp.

OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal
 XX
 XX WO9856808-A1.
 PN
 XX 17-DEC-1998.
 PD
 XX 12-JUN-1998; 98WO-US12334.
 XX
 XX 13-JUN-1997; 97US-0050951.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Blank GS, Narindray DS, Zapata GA;
 PI
 XX WPI; 1999-060267/05.
 DR N-PSDB; AAX03840.
 DR
 XX New method for recovering polypeptides from cell cultures - by
 PT treating with reagent and filtering to remove reagent
 PT
 XX Example; Fig 4; 43pp; English.
 PS
 XX A method has been developed for recovering a polypeptide comprising: (a)
 CC exposing a composition comprising a polypeptide to a reagent which binds
 CC to or modifies the polypeptide, where the reagent is immobilized on a
 CC solid phase; and (b) passing the composition through a filter bearing an
 CC opposite charge to the reagent so as to remove leached reagent from the
 CC composition. The present invention also describes a method for modifying
 CC a precursor antibody comprising a leucine zipper by exposing the
 CC precursor antibody to a protease immobilized on a solid support so that
 CC the protease removes the zipper. The methods can be used to purify
 CC proteins from cell cultures. They are especially useful for isolating
 CC antibodies. The methods overcome the problem of reagent leakage into the
 CC protein as is the case in prior art immobilized modification systems. By
 CC using a opposite charge filter the reagent can be excluded from the
 CC sample, preventing contamination. The present sequence represents the
 CC recombinant humanised anti-CD18 antibody (rhMAB CD18) heavy chain,
 CC which is used in an example from the present invention.
 XX
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1233; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 6.1e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETVTHMMWRQAPGKLEWVAGINPKNGGTSH 60
 DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETVTHMMWRQAPGKLEWVAGINPKNGGTSH 83
 QY 61 NORFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGTILV 120
 DB 84 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGTILV 143
 QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 180
 DB 144 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 203
 QY 181 LQSSGLYSLSVWVTPSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 232
 DB 204 LQSSGLYSLSVWVTPSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 255

RESULT 8
 AAB66785
 ID AAB66785 standard; protein; 300 AA.
 XX
 AC AAB66785;

XX 10-APR-2001 (first entry)
 DT
 XX Protein encoded by ps 1130 expression cassette.
 DE
 XX Antibody; lyophilization; hemorrhagic shock; thermal injury;
 KW myocardial infarction; inflammation.
 XX
 OS Homo sapiens.
 XX
 XX US6171586-B1.
 PN
 XX 09-JAN-2001.
 PD
 XX 12-JUN-1998; 98US-0097171.
 XX
 XX 13-JUN-1997; 97US-0053087.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;
 PI Weissburg RP, Wong RL;
 XX WPI; 2001-136863/14.
 DR
 XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
 PT shock, thermal injury, stroke, and myocardial infarction, comprises an
 PT antibody not subjected to prior lyophilization -
 PT
 XX Disclosure; Fig 21; 56pp; English.
 PS
 XX The present invention relates to a stable aqueous pharmaceutical
 CC formulation, comprising an antibody not subjected to prior
 CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
 CC a polyol. The invention is useful for treating hemorrhagic shock,
 CC thermal injury, e.g. resulting from burns, stroke including
 CC ischemic and hemorrhagic stroke, myocardial infarction,
 CC inflammatory disorders such as adult respiratory distress
 CC syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
 CC arthritis and B-cell lymphomas.
 XX
 SQ Sequence 300 AA;

Query Match 100.0%; Score 1233; DB 22; Length 300;
 Best Local Similarity 100.0%; Pred. No. 6.1e-88;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETVTHMMWRQAPGKLEWVAGINPKNGGTSH 60
 DB 24 EVQLVESGGGLVQPGGSLRLSCATSGYTFETVTHMMWRQAPGKLEWVAGINPKNGGTSH 83
 QY 61 NORFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGTILV 120
 DB 84 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYICARWGLNYGFDVRYFDVWGQGTILV 143
 QY 121 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 180
 DB 144 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 203
 QY 181 LQSSGLYSLSVWVTPSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 232
 DB 204 LQSSGLYSLSVWVTPSSSLGTQTYICNVNHPKSNNTKVDKKVEPKSCDKTHT 255

RESULT 9
 AAB03664
 ID AAB03664 standard; Protein; 537 AA.
 XX
 AC AAB03664;
 XX
 DT 04-OCT-2000 (first entry)
 XX

DE Anti-CD18 antibody (rhUMAB CD18) light and heavy chain protein sequence.
XX Expression cassette: pS1130; rhUMAB CD18; monoclonal antibody;
KW biochemical lysis; polypeptide recovery; anti-CD18 antibody.
XX Synthetic.
XX Key Location/Qualifiers
FH 1..248
FT Region /note= "Anti-CD18 light chain"
FT 249..537
FT Region /note= "Anti-CD18 heavy chain"
XX
XX WO200024873-A1.
XX
XX 04-MAY-2000.
XX
XX 21-OCT-1999; 99WO-US24696.
XX
XX 28-OCT-1998; 98US-0106052.
XX
XX (GETH) GENENTECH INC.
XX Leung WS, Swartz JR;
PI WPI; 2000-350719/30.
XX N-PSDB; AAA53339, AAA53389.
XX
XX Process for large scale production and recovery of polypeptides from
PT bacterial cells using a method of biochemical lysis -
XX
XX Example 1; Fig 4; 64pp; English.
XX
XX This sequence represents the anti-CD18 antibody (rhUMAB CD18) light and
CC heavy chain amino acid sequences. RhUMAB CD18 is a recombinant F(ab')₂
CC antibody, which binds to the MAC-1 (CD11b/CD18) receptor, blocking
CC binding of neutrophils to the endothelium. The expression cassette is
CC used in an example of the process of the invention, for recovering a
CC heterologous polypeptide from bacterial cells using biochemical lysis.
CC The process is used for the large scale production and recovery of
CC polypeptides e.g. human insulin-like growth factor (IGF), DNase, vascular
CC endothelial growth factor (VEGF), anti-CD18 antibody or anti-CD18
CC antibody fragment from bacterial cells.
XX
XX Sequence 537 AA;
SQ
Query Match 100.0%; Score 1233; DB 21; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.2e-87;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWMROAPGKGLEWVAGINPKNGGTS 60
DB 261 evqlvesggglvqp9gslrlscatsgytfeythmwmrqap9gkglewaginpknggtsh 320
QY 61 NQRFMDRFTTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGT 120
DB 321 nqrfmdrftisvdkststaymqmnsraedtavyycarwrglnygfdvryfdvwgqgtlv 380
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
DB 381 tvssastkgpsvfplapssksstsggtaalgclvkdypfpvptvswnsgaltsgvhtfpav 440
QY 181 LOSGLYSLSSVWTVPSSSLGTQTICNVNHNKPSNTKVDKKEPKSCDKTHT 232
DB 441 lqssglyslssvwtvpssslgtqticyicnvnhnkpstkvdkkvepkscdktht 492
RESULT 10
AAW34505
ID AAW34505 standard; protein; 450 AA.
XX
AC AAW34505;

XX 19-MAR-1998 (first entry)
DE Heavy chain of full length IgG2 humanised H52 antibody.
XX
XX Humanised antibody; HuH52; heavy chain; focal ischaemic stroke; embolism;
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;
KW systemic hypoperfusion; cardiac arrest.
XX Synthetic.
OS Homo sapiens.
OS Mus sp.
XX WO9726912-A2.
XX 31-JUL-1997.
PD
XX 11-JAN-1997; 97WO-US00492.
PF
XX 23-JAN-1996; 96US-0589982.
PR
XX (GETH) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX Bednar MM, Gross CE, Thomas GR;
PI WPI; 1997-393373/36.
XX Administering an anti-CD18 antibody to treat focal ischaemic stroke
PT - by increasing cerebral blood flow and reducing size of brain
PT infarct
PS
XX Disclosure; Page 9; 41pp; English.
XX This sequence represents the heavy chain of the humanised H52 antibody.
CC The H52 antibody can be used in the method of the invention. The method
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
CC interrupted blood supply, in a mammal, caused by obstruction of a main
CC cerebral artery, comprises administering anti-CD18 antibody to increase
CC cerebral blood flow and/or reduce the size of the area of brain that
CC dies, without removing the arterial obstruction. CD18, is upregulated in
CC patients after ischaemic stroke or transient ischaemic attack (stroke
CC symptoms last less than 24 hours with complete recovery). Treatment with
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
CC infarct size, improving clinical outcomes in focal ischaemic strokes in
CC mammals, particularly in humans. The method provides an alternative to
CC thrombolytic therapy for treating ischaemic strokes caused by
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
CC therapy has been unsuccessful, is contra-indicated e.g. because such
CC drugs exacerbate bleeding, or is unsuitable because of the time delay
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
CC plasminogen activator) may also be administered before, after or
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
CC be used to treat the third main type of ischaemic stroke, systemic
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
XX
XX Sequence 450 AA;
SQ
Query Match 92.2%; Score 1137; DB 18; Length 450;
Best Local Similarity 94.7%; Pred. No. 2.6e-80;
Matches 215; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMWMROAPGKLEWVAGINPKNGGTS 60
DB 1 evqlvesggglvqp9gslrlscatsgytfeythmwmrqap9gkglewaginpknggtsh 60
QY 61 NQRFMDRFTTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGT 120
DB 61 nqrfmdrftisvdkststaymqmnsraedtavyycarwrglnygfdvryfdvwgqgtlv 120
QY 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180

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Db 121 tvssastkgsfplapcsrstsestaalclvkdypfpvvtvswnsaltsvhtfpav 180
      |||
QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
      |||
Db 181 lqssglyslssvvtvssnftqtytcnvdhkpnsntkvdktverkcc 227
      |||

RESULT 11
AAY08755
ID AAY08755 standard; protein; 450 AA.
XX
AC AAY08755;
XX
DT 10-AUG-1999 (first entry)
XX
DE Human IgG2 huH52 heavy chain protein fragment.
XX
KW IgG; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;
KW CD18 extracellular domain; endothelium; CD18/CD18 complex dissociation;
KW antibody; huH52; heavy chain.
XX
OS Homo sapiens.
XX
PN US5914112-A.
XX
PD 22-JUN-1999.
XX
PF 22-JAN-1997; 97US-0788800.
XX
PR 23-JAN-1996; 96US-0093038.
XX
PR 22-JAN-1997; 97US-0788800.
XX
PA (GETH ) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Bednar MM, Gross CE, Thomas GR;
XX
DR WPI; 1999-370483/31.
XX
PT Anti-CD18 antibodies in stroke
XX
PS Disclosure; Column 31-34; 25pp; English.
XX
CC This invention describes a method for improving the clinical outcome in
CC focal ischaemic stroke by administering novel anti-CD18 antibody which
CC has cerebroprotective properties. The invention particularly describes a
CC method of treating focal ischaemic stroke caused by the obstruction of a
CC main cerebral artery which comprises administering an anti-CD18 antibody
CC to increase the blood flow or reduce the infarct size, where: (1) the
CC antibody binds to an extracellular domain of CD18 and inhibits or reduces
CC the ability of the cell expressing CD18 to bind to endothelium, (2) the
CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the
CC antibody dissociates CD18/CD18 complex. This sequence represents the
CC human IgG 2 huH52 heavy chain region.
XX
SQ Sequence 450 AA;

Query Match 92.2%; Score 1137; DB 20; Length 450;
Best Local Similarity 94.7%; Pred. No. 2.6e-80;
Matches 215; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKGLVWAGINPKNGTSH 60
      |||
Db 1 evqlvesggglvqp9gsirlscatsgytftymhmrqapkgglewvaginpknggtsh 60
      |||

QY 61 NQRFMDRTISVDKSTAYQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLTV 120
      |||
Db 61 nqrfrmdrtisvdkststaymqmnsiraedtavyycarwrglnygfdrvfdvwwggtlv 120
      |||

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QY 121 TVSSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYKPEPEPTVTSWNSGALTSGVHTFPAV 180
      |||
Db 121 tvssastkgsfplapcsrstsestaalclvkdypfpvvtvswnsaltsvhtfpav 180
      |||

QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
      |||
Db 181 lqssglyslssvvtvssnftqtytcnvdhkpnsntkvdktverkcc 227
      |||

RESULT 12
AAR30775
ID AAR30775 standard; protein; 552 AA.
XX
AC AAR30775;
XX
DT 12-MAY-1993 (first entry)
XX
DE pH52-8.0 humanised murine anti-CD18 antibody heavy chain.
KW Humanisation; rapid; monoclonal antibody.
XX
OS Mus musculus.
XX
PN WO9222653-A.
XX
PD 23-DEC-1992.
XX
PF 15-JUN-1992; 92WO-US05126.
XX
PR 14-JUN-1991; 91US-0715272.
XX
PA (GETH ) GENENTECH INC.
XX
PI Carter PJ, Presta LG;
XX
DR WPI; 1993-018139/02.
XX
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
XX
PS Disclosure; Fig 6A; 126pp; English.
XX
CC The sequence is that of the humanised heavy chain sequence of
CC murine anti-CD18 antibody pH52-8.0.
XX
SQ Sequence 552 AA;

Query Match 90.5%; Score 1116; DB 14; Length 552;
Best Local Similarity 93.4%; Pred. No. 1.4e-78;
Matches 212; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFETYMHWMRQAPGKGLVWAGINPKNGTSH 60
      |||
Db 53 evqlvesggglvqp9gsirlscatsgytftymhmrqapkgglewvaginpknggtsh 112
      |||

QY 61 NQRFMDRTISVDKSTAYQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLTV 120
      |||
Db 113 nqrfrmdrtisvdkststaymqmnsiraedtavyycarwrglnygfdrvfdvwwggtlv 172
      |||

QY 121 TVSSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYKPEPEPTVTSWNSGALTSGVHTFPAV 180
      |||
Db 173 tvssastkgsfplapcsrstsestaalclvkdypfpvvtvswnsaltsvhtfpav 232
      |||

QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 227
      |||
Db 233 lqssglyslssvvtvssnftqtytcnvdhkpnsntkvdktverkcc 279
      |||

RESULT 13
AAW00374
ID AAW00374 standard; Protein; 232 AA.
XX

```

AC AAW00374;
 XX 24-JAN-1997 (first entry)
 XX
 XX
 DE Anti-CD18 chimeric antibody MHM23 heavy chain.
 XX
 XX Antibody purification; low pH hydrophobic interaction chromatography;
 KW monoclonal antibody; chimeric antibody; humanised antibody; MHM23;
 KW heavy chain.
 XX
 XX Synthetic.
 OS
 XX WO9633208-A1.
 PN
 XX 24-OCT-1996.
 PD
 XX 05-APR-1996; 96WO-US04683.
 XX
 XX 20-APR-1995; 95US-0425763.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Rinderknecht EH, Zapata GA;
 XX
 XX WPI; 1996-485726/48.
 DR
 XX Antibody purification by low pH hydrophobic interaction
 PT chromatography - allows isolation of correctly folded and
 PT disulphide bonded antibodies
 XX
 XX Example 1; Page 26-27; 41pp; English.
 PS
 XX The heavy chain (AAW00374) and light chain (AAW00373) of a chimeric
 CC version of anti-CD18 monoclonal antibody MHM23 were used to
 CC demonstrate a novel technique for antibody purification. Low pH
 CC hydrophobic interaction chromatography provides for the purification
 CC of correctly-folded and disulphide-bonded antibody fragments from
 CC unwanted contaminants. The antibody compsns. obtd. are at least 95%
 CC pure.
 XX
 XX Sequence 232 AA;
 SQ
 Query Match 88.7%; Score 1094; DB 17; Length 232;
 Best Local Similarity 86.2%; Pred. No. 2.7e-77;
 Matches 200; Conservative 17; Mismatches 15; Indels 0; Gaps 0;
 QY 1 EVLVESGGGLVOPGSLRLSCATSGYTFETVTHMWRQAPGKGLWVAGINPKNGTSH 60
 Db 1 evlqggpelvkgpgavsktsksgytfetymhmwrqshgkslewlggnpknngssh 60
 QY 61 NQRFMDRFTISVDKSTSTAYMOMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
 Db 61 nqrfmdkatlavdkststaymelrsltsedsgiyycarwrglnygfdrvfdvwgagttv 120
 QY 121 TVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 180
 Db 121 tvssastkgpsvflapsskstsrgtaalgclvkdypfpvtsvwnsgaltsgvhtfpav 180
 QY 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHT 232
 Db 181 lqssgylslsvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232
 RESULT 14
 AAR30774
 ID AAR30774 standard; protein; 454 AA.
 XX
 XX AAR30774;
 XX
 XX 12-MAY-1993 (first entry)
 DT
 XX H52H4-160 murine anti-CD18 antibody heavy chain.
 DE

XX Humanisation; rapid; monoclonal antibody.
 KW
 XX Mus musculus.
 OS
 XX WO9222653-A.
 PN
 XX 23-DEC-1992.
 PD
 XX 15-JUN-1992; 92WO-US05126.
 PF
 XX 14-JUN-1991; 91US-0715272.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Carter PJ, Presta LG;
 PI
 XX WPI; 1993-018139/02.
 DR
 XX Humanisation of antibodies - by molecular modelling of the variable
 PT domains and alteration by gene conversion mutagenesis
 PT
 XX Disclosure; Fig 6A; 126pp; English.
 PS
 XX The sequence is that of the heavy chain of murine anti-CD18
 CC antibody H52H4-160.
 CC
 XX Sequence 454 AA;
 SQ
 Query Match 88.5%; Score 1091; DB 14; Length 454;
 Best Local Similarity 85.8%; Pred. No. 9.8e-77;
 Matches 199; Conservative 18; Mismatches 15; Indels 0; Gaps 0;
 QY 1 EVLVESGGGLVOPGSLRLSCATSGYTFETVTHMWRQAPGKGLWVAGINPKNGTSH 60
 Db 1 evlqggpelvkgpgavsktsksgytfetymhmwrqshgkslewlggnpknngssh 60
 QY 61 NQRFMDRFTISVDKSTSTAYMOMNSLRADTAVYYCARWRGLNYGFDVRYFDVWGOGTLV 120
 Db 61 nqrfmdkatlavdkststaymelrsltsedsgiyycarwrglnygfdrvfdvwgagttv 120
 QY 121 TVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAV 180
 Db 121 tvssastkgpsvflapsskstsrgtaalgclvkdypfpvtsvwnsgaltsgvhtfpav 180
 QY 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHT 232
 Db 181 lqssgylslsvvtvpssslgtqtyicnvnhkpsntkvdkkvepkscdktht 232
 RESULT 15
 AAY29444
 ID AAY29444 standard; Protein; 253 AA.
 XX
 XX AAY29444;
 AC
 XX 05-OCT-1999 (first entry)
 DT
 XX Humanised anti-IL-8 6G4.2.5vll heavy chain and STII leader peptide.
 DE
 XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
 KW diagnosis; inflammatory disorder; conjugate; immunoglobulin;
 KW fusion protein.
 KW
 XX Synthetic.
 OS
 XX Mus musculus.
 OS
 XX Homo sapiens.
 OS
 XX WO9937779-A1.
 PN
 XX 29-JUL-1999.
 PD
 XX

```
PF 19-JAN-1999; 99WO-US01081.
XX
PR 24-JUL-1998; 98US-0122513.
PR 22-JAN-1998; 98US-0012116.
PR 20-FEB-1998; 98WO-US03337.
PR 24-JUL-1998; 98US-0121952.
XX
PA (GETH ) GENENTECH INC.
XX
PI Hsei V, Koumenis I, Leong SJ, Presta LG, Shahroksh Z;
PI Zapata GA;
XX
DR WPI; 1999-469134/39.
XX
PT New conjugates of nonproteinaceous polymers with antibody fragments,
PT used for treating inflammatory disorders
XX
PS Example; Fig 31; 36Opp; English.
XX
CC The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischaemic
CC reperfusion disorder, and autoimmune diseases. They can also be used
CC for treating e.g. inflammatory skin diseases including psoriasis and
CC atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic
CC diseases. The conjugates can also be used as reagents in an animal
CC model system for in vivo study of the biological functions of the
CC antigen recognised by the conjugate. The present sequence represents
CC the humanised anti-IL-8 664.2.5 heavy chain in an N-terminal fusion
CC with the STII leader peptide from the present invention.
XX
SQ Sequence 253 AA;
```

Query Match 83.5%; Score 1030; DB 20; Length 253;
Best Local Similarity 84.0%; Pred. No. 2.7e-72;
Matches 199; Conservative 12; Mismatches 14; Indels 12; Gaps 2;

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QY 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTHMMROAPGKGLEWVAGINPKNGGTS 60
Db 24 evqlvqsgggivqp9gsirlscasgysfssymhwvrgapkglewgyiopsngetty 83
QY 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRY-----EDVMG 115
Db 84 nqkfkgftlrdnsnkntaylqmnsdraedtavyycarg-----dyryngdwffdvwg 136
QY 116 QGTLVTSSASTKGPSVTPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVH 175
Db 137 qgtlvtvssastkgpsvfpapsskstsggtaalgclvkdypfpvptvswnsgaltsgvh 196
QY 176 TFPVAVLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKVEPKSCDKTHT 232
Db 197 tfpavlgssglyslssvvtpvpssslgtqtyicnvnhkpsntkvdkkvpeksckdtkht 253
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Search completed: August 14, 2002, 11:00:45
Job time: 526 sec

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OM protein - protein search, using sw model

Run on: August 14, 2002, 10:57:15 ; Search time 20.83 seconds
(without alignments)
272.047 Million cell updates/sec

Title: US-09-811-384-10
Perfect score: 1233
Sequence: 1 EVQLVESGGGLVPGGSLRL.....PSNKTVDKVEPKSCDKTHT 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	100.0	232	2	US-07-934-373C-29
2	1233	100.0	232	2	US-08-788-800-10
3	1233	100.0	232	3	US-08-437-642B-29
4	1233	100.0	232	5	PCT-US93-07832-29
5	1233	100.0	235	2	US-07-934-373C-30
6	1233	100.0	235	3	US-08-437-642B-30
7	1233	100.0	235	5	PCT-US93-07832-30
8	1233	100.0	241	3	US-09-097-309-1
9	1233	100.0	241	4	US-09-097-171A-1
10	1233	100.0	300	3	US-09-097-309-7
11	1233	100.0	300	4	US-09-097-171A-11
12	1233	100.0	300	4	US-09-422-712B-3
13	1233	100.0	300	4	US-09-607-756-3
14	1216	98.6	232	2	US-07-934-373C-27
15	1216	98.6	232	3	US-08-437-642B-27
16	1216	98.6	232	5	PCT-US93-07832-27
17	1211	98.2	232	2	US-07-934-373C-28
18	1211	98.2	232	3	US-08-437-642B-28
19	1211	98.2	232	5	PCT-US93-07832-28
20	1207	97.9	232	2	US-07-934-373C-31
21	1207	97.9	232	2	US-07-934-373C-38
22	1207	97.9	232	3	US-08-437-642B-31
23	1207	97.9	232	3	US-08-437-642B-38
24	1207	97.9	232	5	PCT-US93-07832-31
25	1207	97.9	232	5	PCT-US93-07832-38
26	1206	97.8	232	2	US-07-934-373C-35
27	1206	97.8	232	2	US-07-934-373C-36

28	1206	97.8	232	3	US-08-437-642B-35	Sequence 35, Appl
29	1206	97.8	232	3	US-08-437-642B-36	Sequence 36, Appl
30	1206	97.8	232	5	PCT-US93-07832-35	Sequence 35, Appl
31	1206	97.8	232	5	PCT-US93-07832-36	Sequence 36, Appl
32	1205	97.7	232	2	US-07-934-373C-33	Sequence 33, Appl
33	1205	97.7	232	3	US-08-437-642B-33	Sequence 33, Appl
34	1205	97.7	232	5	PCT-US93-07832-33	Sequence 33, Appl
35	1198	97.2	232	2	US-07-934-373C-32	Sequence 32, Appl
36	1198	97.2	232	3	US-08-437-642B-32	Sequence 32, Appl
37	1198	97.2	232	5	PCT-US93-07832-32	Sequence 32, Appl
38	1195	96.9	232	2	US-07-934-373C-37	Sequence 37, Appl
39	1195	96.9	232	3	US-08-437-642B-37	Sequence 37, Appl
40	1195	96.9	232	5	PCT-US93-07832-37	Sequence 37, Appl
41	1191	96.6	232	2	US-07-934-373C-34	Sequence 34, Appl
42	1191	96.6	232	3	US-08-437-642B-34	Sequence 34, Appl
43	1191	96.6	232	5	PCT-US93-07832-34	Sequence 34, Appl
44	1171	95.0	232	2	US-07-934-373C-26	Sequence 26, Appl
45	1171	95.0	232	3	US-08-437-642B-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-07-934-373C-29
; Sequence 29, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-29

Query Match 100.0%; Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
Db 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
QY 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAIVYCARWRGLNYGFDVRYFDVWGOGTLV 120
Db 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAIVYCARWRGLNYGFDVRYFDVWGOGTLV 120
QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180
Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180
QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232
RESULT 2
US-08-788-800-10
; Sequence 10, Application us/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-10

Query Match 100.0%; Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
Db 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
QY 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAIVYCARWRGLNYGFDVRYFDVWGOGTLV 120
Db 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAIVYCARWRGLNYGFDVRYFDVWGOGTLV 120
QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180
Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180

Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180
QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKEPKSCDKTHT 232
RESULT 3
US-08-437-642B-29
; Sequence 29, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-29

Query Match 100.0%; Score 1233; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
Db 1 EVOLVESGGLVQPGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
QY 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAIVYCARWRGLNYGFDVRYFDVWGOGTLV 120
Db 61 NORFMDRTTISVDKSTSTAYMQMNSLRADTAIVYCARWRGLNYGFDVRYFDVWGOGTLV 120
QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180
Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVHHTFPV 180

Db 121 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPV 180
QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232
RESULT 4
PCT-US93-07832-29
; Sequence 29, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-29
Query Match 100.0%; Score 1233; DB 5; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVOPGGSRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
QY 61 NQRFMDRTTISVDKSTAYMQMNSLRAEDTAVYICARWGLNYGDFVYFDVWGQGLV 120
Db 61 NQRFMDRTTISVDKSTAYMQMNSLRAEDTAVYICARWGLNYGDFVYFDVWGQGLV 120
QY 121 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPV 180
Db 121 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPV 180
QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232

Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232
RESULT 5
US-07-934-373C-30
; Sequence 30, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-30
Query Match 100.0%; Score 1233; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVOLVESGGGLVOPGGSRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
Db 1 EVOLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKLEWVAGINPKNGGTS 60
QY 61 NQRFMDRTTISVDKSTAYMQMNSLRAEDTAVYICARWGLNYGDFVYFDVWGQGLV 120
Db 61 NQRFMDRTTISVDKSTAYMQMNSLRAEDTAVYICARWGLNYGDFVYFDVWGQGLV 120
QY 121 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPV 180
Db 121 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPV 180
QY 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 232
RESULT 6
US-08-437-642B-30
; Sequence 30, Application US/08437642B

Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709p2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-30

Query Match 100.0%; Score 1233; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYFTFTYTHMMRQAPGKGLVWAGINPKNGGTS 60
Db 1 EVLVESGGGLVQPGGSLRLSCATSGYFTFTYTHMMRQAPGKGLVWAGINPKNGGTS 60

QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120
Db 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120

QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 180

QY 181 LQSSGLYSLSVVTPVPSLSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSVVTPVPSLSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 232

RESULT 7
PCT-US93-07832-30
; Sequence 30, Application PC/TUS9307882

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-30

Query Match 100.0%; Score 1233; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 4.4e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCATSGYFTFTYTHMMRQAPGKGLVWAGINPKNGGTS 60
Db 1 EVLVESGGGLVQPGGSLRLSCATSGYFTFTYTHMMRQAPGKGLVWAGINPKNGGTS 60

QY 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120
Db 61 NQRFMDRTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120

QY 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 180

QY 181 LQSSGLYSLSVVTPVPSLSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSVVTPVPSLSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 232

RESULT 8
US-09-097-309-1
; Sequence 1, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-Jun-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-309-7

Query Match 100.0%; Score 1233; DB 3; Length 300;
Best Local Similarity 100.0%; Pred. No. 6e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 60
Db 24 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 83
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 120
Db 84 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 143
QY 121 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 144 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 203
QY 181 LQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSN TKVDKKVEPKSCDKTHT 232
Db 204 LQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSN TKVDKKVEPKSCDKTHT 255

RESULT 11
US-09-097-171A-11
Sequence 11, Application US/09097171A
Patent No. 6171586
GENERAL INFORMATION:
APPLICANT: Lam, Xanthe M.
APPLICANT: Oeswein, James Q.
APPLICANT: Ongipattanakul, Boonsri
APPLICANT: Shahrokh, Zahra
APPLICANT: Wang, Sharon X.
APPLICANT: Weissburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-11

Query Match 100.0%; Score 1233; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 6e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 60
Db 24 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 83
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 120
Db 84 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 143
QY 121 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
Db 144 TVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 203
QY 181 LQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSN TKVDKKVEPKSCDKTHT 232
Db 204 LQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSN TKVDKKVEPKSCDKTHT 255

RESULT 12
US-09-422-712B-3
Sequence 3, Application US/09422712B
Patent No. 6180367
GENERAL INFORMATION:
APPLICANT: Leung, Woon-Lam Susan
APPLICANT: Swartz, James R.
TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
FILE REFERENCE: P1711R1
CURRENT APPLICATION NUMBER: US/09/422,712B
CURRENT FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTH: 300
TYPE: PRT
ORGANISM: Human
US-09-422-712B-3

Query Match 100.0%; Score 1233; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 6e-100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 60
Db 24 EVLVESGGGLVQPGGSLRLSCATSGYTFEYTMHMRQAPGKGLEWVAGINPKNGTSH 83
QY 61 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 120
Db 84 NQRFMDRFTISVDKSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLV 143

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/05126
;; FILING DATE: 15-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/15272
;; FILING DATE: 14-JUN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709P2C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 27:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 232 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-437-642B-27

Query Match 98.6%; Score 1216; DB 3; Length 232;
Best Local Similarity 98.3%; Pred. No. 1.3e-98;
Matches 228; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHWMRQAPGKGLWVAGINPKNGGTSH 60
Db 1 EVQLVESGGGLVQPGGSLRLSCATSGYTFEYTMHWMRQAPGKGLWVAGINPKNGGTSH 60
Qy 61 NQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120
Db 61 NQRFMDRFTISVDKSKNTLYLQMNLSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGLV 120
Qy 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
Qy 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232
Db 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT 232

Search completed: August 14, 2002, 11:01:12
Job time: 237 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 11:05:26 ; Search time 29.5 Seconds
(without alignments)
697.055 Million cell updates/sec

Title: US-09-811-384-11
Perfect score: 1118
Sequence: 1 DIQMTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	938.5	83.9	215	2 JE0244	Ig kappa chain NIG
2	934.5	83.6	215	2 JE0242	Ig kappa chain NIG
3	916.5	82.0	215	2 JE0243	Ig kappa chain NIG
4	869.5	77.8	215	2 A23746	Ig kappa chain V-I
5	843	75.4	216	2 JE0241	Ig kappa chain Am3
6	758	67.8	230	2 S33161	Ig kappa chain - s
7	736	65.8	234	2 S14237	Ig kappa chain pre
8	735	65.7	240	2 S06084	Ig kappa chain pre
9	718	64.2	220	2 A31790	Ig kappa chain V r
10	717	64.1	234	2 S01320	Ig kappa chain pre
11	707.5	63.3	219	2 S52028	Ig kappa chain - m
12	703	62.9	218	2 S68241	Ig kappa chain v r
13	701	62.7	218	2 JC5810	monoclonal antibod
14	700.5	62.7	219	2 PC4203	Ig kappa chain (mo
15	697.5	62.4	225	2 S37484	Ig kappa chain - m
16	694	62.1	214	2 S68212	Ig kappa chain (Ma
17	693.5	62.0	219	2 S38865	Ig kappa chain - m
18	691.5	61.9	217	2 S42772	Ig kappa chain - m
19	684.5	61.2	235	2 S25058	Ig kappa chain - m
20	680.5	60.9	219	2 S16112	Ig kappa chain v r
21	669	59.8	210	2 A56169	Ig kappa chain V r
22	667.5	59.7	225	2 JL0029	Ig kappa chain pre
23	612.5	54.8	135	2 S52059	JC-kappa protein -
24	586	52.4	178	2 PT0219	Ig kappa chain V-C
25	581.5	52.0	229	2 A20969	Ig kappa chain pre
26	548	49.0	106	1 K3HU	Ig kappa chain C r
27	528.5	47.3	238	2 A49633	Ig lambda-like cha
28	513	45.9	99	2 A37927	Ig kappa chain C r
29	507	45.3	99	2 S26653	Ig kappa chain C r

30	506.5	45.3	197	2 S29593	Ig kappa chain (WM
31	499	44.6	127	2 S40367	Ig kappa chain V-J
32	496	44.4	139	2 S40365	Ig kappa chain - h
33	491	43.9	141	2 A49134	Ig kappa chain V-I
34	487	43.6	123	2 S40331	Ig kappa chain - h
35	484	43.3	108	2 B49047	Ig kappa chain V r
36	484	43.3	131	2 S40352	Ig kappa chain V-J
37	482	43.1	122	2 S40314	Ig kappa chain - h
38	481	43.0	132	2 S40334	Ig kappa chain - h
39	480	42.9	108	2 S19674	Ig kappa chain V r
40	476.5	42.6	124	2 S40336	Ig kappa chain V-J
41	476	42.6	144	2 PL0106	Ig kappa chain pre
42	475	42.5	109	2 S31981	Ig kappa chain - h
43	474	42.4	108	1 KJHULY	Ig kappa chain V-I
44	474	42.4	130	2 S40368	Ig kappa chain - h
45	473	42.3	129	2 S40317	Ig kappa chain - h

ALIGNMENTS

RESULT 1

JE0244

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 938.5; DB 2: Length 215;
Best Local Similarity 83.7%; Pred. No. 1.4e-55;
Matches 180; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

Qy	1	DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS	60
Db	1	EVLTQSPATLSVSPGERATLSCRASQSVHSLAWYQKPGQAPRLLIYRSTRATGIPA	60
Qy	61	RFGSGSGTDYTLTISSLPEDFATYYCOQGNLPP-TEGQGTKEIKRTVAAPSVFIEP	119
Db	61	RFGSGSGTDFTLTITSSLSQSEDFALYCOQYNTWPTLTTEGGGTKEIKRTVAAPSVFIEP	120
Qy	120	PSDEQLKSGTASVWCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL	179
Db	121	PSDEQLKSGTASVWCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTL	180
Qy	180	TLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	214
Db	181	TLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

submitted to JIPID, November 1998

A:Description: Structure relationship of kappa type light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Db 61 EGVDPDRFTGSGGSDTFTLTITSSVQAEADLAVYYCONDYSNPLTFGGGTYKLELKRADAAPT 120

QY 115 VFIPPPDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYSTS 174

Db 121 VSIFPPSSSEQLTSGGASVYVCLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKDSYSTS 180

QY 175 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214

Db 181 MSSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 220

RESULT 10

S01320

Ig kappa chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000

C:Accession: S01320

R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fliers, W.

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a

A:Reference number: S01320; MUID:88329081

A:Accession: S01320

A:Molecule type: mRNA

A:Residues: 1-234 <DE1>

A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785

A:Note: this sequence was determined from the differentiated gene

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-234/Product: Ig kappa chain #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 717; DB 2; Length 234;

Best Local Similarity 63.6%; Pred. No. 7.6e-41;

Matches 136; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 21 DIQMTQSPASLSVSGESVITTCRASNIYSLAWYQKQKSPQLLYVYATKLVGVPS 80

QY 61 RFSGSGSGTDYTLTISSLQPEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPSFIPTP 120

Db 81 RFSGSGSGTDYTLKINSLSLQPEDFATYYCOQGNLTPPTFGSGTKLEMKRADAAPTIVSIFPP 140

QY 121 SDQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYSTLSSTLT 180

Db 141 SSQLTSGGASVYVCLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKDSYSTLSSTLT 200

QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214

Db 201 LTRKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 11

S52028

Ig kappa chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S52028

R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;

submitted to the EMBL Data Library, August 1994

A:Description: Coordinate expression of antibody subunit genes yields high levels of fur

A:Reference number: S52028

A:Accession: S52028

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-219 <VAN>

A:Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 707.5; DB 2; Length 219;

Best Local Similarity 60.7%; Pred. No. 3e-40;

Matches 133; Conservative 29; Mismatches 52; Indels 5; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLH 55

Db 1 DVMVTQSPSLPVLGDDQASISCRSSQSIHVSNGNTYLEMYLQKPGQSPKLLIYKVSNR 60

QY 56 SGVPRFSGSGGTDTLTITSLQPEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 115

Db 61 SGVPRFSGSGGTDTLTLSRVEADLGVYCFQGSHPPTFGGNTLEIKRADAAPT 120

QY 116 FIFPPSDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYSTL 175

Db 121 SIFPPSSEQLTSGGASVYVCLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKDSYSTSM 180

QY 176 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214

Db 181 SSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 219

RESULT 12

S68241

Ig kappa chain V region (Mab13-1) - mouse (fragment)

N:Alternate names: immunoglobulin light chain

C:Species: Mus musculus (house mouse)

C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S68241; S68214

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,

submitted to the EMBL Data Library, March 1994

A:Description: Specific peroxidase activity by formation of an antibody L-chain-porph

A:Reference number: S68241

A:Accession: S68241

A:Molecule type: mRNA

A:Residues: 1-218 <TAK>

A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BA06141.1; PID:g473963

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,

FBBS Lett. 375, 273-276, 1995

A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr

A:Reference number: S68211; MUID:96085223

A:Accession: S68214

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 'NI', 3-212 <TAW>

A:Cross-references: EMBL:D29670

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 62.9%; Score 703; DB 2; Length 218;

Best Local Similarity 59.6%; Pred. No. 6e-40;

Matches 130; Conservative 35; Mismatches 49; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNLYNWYQKPGKAPKLLIYYTSTLH 56

Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGKAPKLLISLATNLES 60

QY 57 GVPSRFSGSGGTDTLTITSLQPEDFATYYCOQGNLTPPTFGQGTKEIKRTVAAPS 116

Db 61 GVPARFSGSGGTDTLTINHPVEEDVATYYCQHSRELPLTFGAGTKLEKRAADAAPT 120

QY 117 FIFPPSDEQLKSGTASVYVCLNNFYPREAKVQKVDNALQSGNSQBSVTEQDSKDSYSTLS 176

Db 121 FIFPPSSEQLTSGGASVYVCLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKDSYSTSM 180

QY 177 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214

Db 181 SFTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 218

RESULT 13

JC5810

monoclonal antibody 13-1 light chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JCS810

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A:Reference number: JCS810; MUID:98063277

A:Accession: JCS810

A:Molecule type: protein

A:Residues: 1-218 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 62.7%; Score 701; DB 2; Length 218;

Best Local Similarity 60.1%; Pred. No. 8.2e-40;

Matches 131; Conservative 33; Mismatches 50; Indels 4; Gaps 1;

Qy 1 DIOMTQSPSLSASVGDRTITCRASQDINN----YLNWYQKPGKAPKLLIYYTSLHS 56

Db 1 NIVLTQSPASLAVSLGORATISCRASKSVSASGYIYMHYQKPGQPKLLISLNSLES 60

Qy 57 GVPSPRSFGSGGTDYTLTISSLOPEDFATYYCOQGNLTLPTEFGOGTKVEIKRTVAAPSVF 116

Db 61 GVPARESGSGGTDFTLNTHPVEEDVATYYCOHSRELPLTFGAGTKLEKRAADAAPTVS 120

Qy 117 IFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176

Db 121 IFPPSDEQLTSGGASVCLNNFYPRKIDINVKWKIDGSRQNGVLNWTQDQSKDSTYSMS 180

Qy 177 STLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 214

Db 181 STLTLTDEYERHNSYTCETHKTSPIVKSFNRNEC 218

RESULT 14

PC4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C:Accession: PC4203

R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody

A:Reference number: PC4202; MUID:97082978

A:Accession: PC4203

A:Molecule type: mRNA

A:Residues: 1-219 <KWA>

C:Cross-references: GB:U29147; NID:g1594225; PIDN:AA52821.1; PID:g1594226

C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:1-112/Domain: V region #status predicted <VRG>

F:113-219/Domain: C region #status predicted <CRG>

Query Match 62.7%; Score 700.5; DB 2; Length 219;

Best Local Similarity 60.3%; Pred. No. 8.7e-40;

Matches 132; Conservative 30; Mismatches 52; Indels 5; Gaps 1;

Qy 1 DIOMTQSPSLSASVGDRTITCRASQDI-----NNYLNWYQKPGKAPKLLIYYTSLH 55

Db 1 DVLMTQTLPLSPVSLGDAQSISCRSSQSIHTNGNTVLEWYLOKPGQSPKLLIYKVSNR 60

Qy 56 SGVPSRFSFGSGGTDYTLTISSLOPEDFATYYCOQGNLTLPTEFGOGTKVEIKRTVAAPSV 115

Db 61 SGVPSRFSFGSGGTDYTLTISSRVEADLVGYCYFCQGSHPVPTFGGKTKLEIKRAADAAPT 120

Qy 116 FTTPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 175

Db 121 STFPSPSEQLTSGGASVCLNNFYPRKIDINVKWKIDGSRQNGVLNWTQDQSKDSTYSM 180

Qy 176 SSTLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 214

Db 181 SSTLTLTDEYERHNSYTCETHKTSPIVKSFNRNEC 219

RESULT 15

S37484

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C:Accession: S37484

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37484

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-225 <DUG>

A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 62.4%; Score 697.5; DB 2; Length 225;

Best Local Similarity 61.5%; Pred. No. 1.4e-39;

Matches 131; Conservative 32; Mismatches 49; Indels 1; Gaps 1;

Qy 2 IOMTQSPSLSASVGDRTITCRASQDINNYLNWYQKPGKAPKLLIYYTSLHGVPSR 61

Db 14 IVMTQTPKFLLLSAGDRVTITCKASQSVSNVAVYQKPGQSPKLLIYASSRYTGVDPDR 73

Qy 62 FSGSGSGTDYTLTISSLOPEDFATYYCOQGNLTLPTEFGOGTKVEIKRTVAAPSVFIFFPS 121

Db 74 FTGSGYGTDTFTISTVQAEDLAVYFCQDYS-SYTFGGGTKEIKRAADAAPTVSIFPPS 132

Qy 122 DEOLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLTFL 181

Db 133 SEQLTSGGASVCLNNFYPRKIDINVKWKIDGSRQNGVLNWTQDQSKDSTYSMSSTLTFL 192

Qy 182 SKADYKHKVACEVTHQGLSSPVTKSFNRGEC 214

Db 193 TKDEYERHNSYTCETHKTSPIVKSFNRNEC 225

Search completed: August 14, 2002, 11:05:26

Job time: 361 sec

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	548	49.0	106	1	KVJM_HUMAN	P01834	homo sapien
2	474	42.4	108	1	KVJH_HUMAN	P01605	homo sapien
3	470	42.0	108	1	KVJH_HUMAN	P01600	homo sapien
4	468	41.9	108	1	KV5O_MOUSE	P01648	mus musculus
5	467	41.8	108	1	KVJY_HUMAN	P80362	homo sapien
6	466	41.7	108	1	KVJH_HUMAN	P01594	homo sapien
7	466	41.7	108	1	KV5B_MOUSE	P01647	mus musculus
8	464	41.5	108	1	KV1Q_HUMAN	P01607	homo sapien
9	463	41.4	108	1	KV1A_HUMAN	P01593	homo sapien
10	463	41.4	108	1	KV5K_MOUSE	P01644	mus musculus
11	461	41.2	108	1	KV5L_MOUSE	P01645	mus musculus
12	459	41.1	108	1	KV1V_HUMAN	P04430	homo sapien
13	459	41.1	129	1	KV1W_HUMAN	P04431	homo sapien
14	456	40.8	108	1	KV1E_HUMAN	P01597	homo sapien
15	456	40.8	108	1	KV1P_HUMAN	P01608	homo sapien
16	456	40.8	108	1	KV5M_MOUSE	P01646	mus musculus
17	455	40.7	108	1	KV1N_HUMAN	P01606	homo sapien
18	453	40.5	108	1	KV1G_HUMAN	P01599	homo sapien
19	451	40.3	108	1	KV1S_HUMAN	P01611	homo sapien
20	447	40.0	108	1	KV1F_HUMAN	P01598	homo sapien
21	447	40.0	108	1	KV1R_HUMAN	P01610	homo sapien
22	446	39.9	108	1	KV1Q_HUMAN	P01609	homo sapien
23	445	39.8	108	1	KV1K_HUMAN	P01603	homo sapien
24	443.5	39.7	107	1	KV1D_HUMAN	P01596	homo sapien
25	442	39.5	108	1	KV5J_MOUSE	P01643	mus musculus
26	440	39.4	108	1	KV1L_HUMAN	P01604	homo sapien
27	440	39.4	108	1	KV5U_MOUSE	P04946	mus musculus
28	436	39.0	108	1	KV1C_HUMAN	P01595	homo sapien
29	435.5	39.0	109	1	KV1T_HUMAN	P01612	homo sapien
30	425	38.0	129	1	KV1S_HUMAN	P04432	homo sapien
31	408	36.5	108	1	KV5P_MOUSE	P01649	mus musculus
32	408	36.5	117	1	KV1J_HUMAN	P01602	homo sapien
33	403	36.2	117	1	KV1I_HUMAN	P01601	homo sapien

```

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; J00241; AAA58989.1; -
DR EMBL; V00557; CAA23823.1; -
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR MIM; 147200; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIG-VAR_003897.
FT D -> N (IN REF. 7 AND 8).
FT E -> O (IN REF. 5 AND 6).
FT CONFLICT 14 14
FT CONFLICT 57 57
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 49.0%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.8e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 TVAAPSVFIFFPSDQLKSGTASVCLLNFFPREAKVQKVDNALQSGNSQESVTEQDS 168
Db 1 TVAAPSVFIFFPSDQLKSGTASVCLLNFFPREAKVQKVDNALQSGNSQESVTEQDS 60
QY 169 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 2
KV1M_HUMAN
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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[1]
RN SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; K1HULY.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 42.4%; Score 474; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 1e-32;
Matches 90; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNYLNQYQKPGKAPKLLIYYTSLHSGVPS 60
Db 1 DIQMTQSPSSLSVSGDRVTITCQASQNVNAYLNQYQKPGKAPKLLIYGASTREAGVPS 60
QY 61 RFGSGSGTDTLTITSLQPEDFATYYCQGNLPTPTFGQGTKEVTKR 108
Db 61 RFGSGSGTDTFTTITSLQPEDIATYYCQYNNWPPPTFGQGTKEVTKR 108

RESULT 3
KV1H_HUMAN
ID KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1HUHU.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.

```

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 42.0%; Score 470; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 2.2e-32;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCRASQSSYLSWYQKPGKAPQVLIYAASLPSGVPS 60

Qy 61 RFSGSGSDTYLTISLQPEDFATYYCQGNLTLPPTFGQGTKEIKR 108

Db 61 RFSGSGSDTYLTISLQPEDFATYYCQNYITPFSFGQGTKEIKR 108

RESULT 4

ID KV50_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RA Siegelman M., Capra J.D.;
RX MEDLINE=82150934; PubMed=6801658;
RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KMSAR.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 41.9%; Score 468; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 3.2e-32;
Matches 88; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Qy 61 RFSGSGSDTYLTISLQPEDFATYYCQGNLTLPPTFGQGTKEIKR 108

Db 61 RFSGSGSDTYLTISLQPEDISTYFCQGNALPRTFGGKTKEIKR 108

RESULT 5

KV1Y_HUMAN
ID KV1Y_HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RX Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M.;
RA "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers.";
RT Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RX Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M., Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-related fragment of the human kappa Bence Jones protein Wat.";
J. Mol. Biol. 147:185-193(1981).
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PDB; 1WTL; 01-NOV-94.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 41.8%; Score 467; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 3.8e-32;
Matches 89; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDITVYNNVQRPQGPQAPKVIYGSILETGVP 60

Qy 61 RFSGSGSDTYLTISLQPEDFATYYCQGNLTLPPTFGQGTKEIKR 108

Db 61 RFSGSGSDTYLTISLQPEDIATYYCQYDTLPLTEGGGKTKEIKR 108

RESULT 6

KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)


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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR: A01862; KIHUAU.
DR HSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6F6B9 CRC64;

Query Match 41.7%; Score 466; DB 1; Length 108;
Best Local Similarity 84.3%; Pred. No. 4.7e-32;
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYDASNLESGVPS 60

Qy 61 RFSGSGSGFTDYITLTISSLOPEDFATYCCQGNLPTPTFGGQTKVEIKR 108
Db 61 RFSGSGSGAHEFTTISLSLOPEDATYCCQYDYLPTWTFGGQTKVEIKR 108

RESULT 7
KV5N_MOUSE
ID KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-V region HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
ON NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
CC PIR: A01927; KVMKAR.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match 41.7%; Score 466; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 4.7e-32;
Matches 89; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Qy 61 RFSGSGSGTDYITLTISLSLOPEDFATYCCQGNLPTPTFGGQTKVEIKR 108
Db 61 RFSGSGSGTDYSLTISLNLEQEDATYFCQGGKTLPTFTGGGTKLEIKR 108

RESULT 8
KV10_HUMAN
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0 A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

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PIR; A01873; KIHURE.
DR PDB; 1REI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BCE2A CRC64;

Query Match 41.5%; Score 464; DB 1; Length 108;
Best Local Similarity 83.3%; Pred. No. 6.8e-32;
Matches 90; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
|||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
|||||
QY 61 RFSGSGSDTYTLTISSLPQEDFATYCCQGNTPPTFGQGTKEIKR 108
|||||
DB 61 RFSGSGSDTYTLTISSLPQEDFATYCCQXQSLPYTFGQGTKEIKR 108
|||||

RESULT 9
KVIA_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01861; KIHUAG.

HSP: P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 41.4%; Score 463; DB 1; Length 108;
Best Local Similarity 82.4%; Pred. No. 8.2e-32;
Matches 89; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
|||||
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
|||||
QY 61 RFSGSGSDTYTLTISSLPQEDFATYCCQGNTPPTFGQGTKEIKR 108
|||||
DB 61 RFSGSGSDTYTLTISSLPQEDFATYCCQYDTLPRTFGQGTKEIKR 108
|||||

RESULT 10
KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-V region HP R16.7.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idio type.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Antiarsenate antibody.

FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;

Query Match 41.4%; Score 463; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 8.2e-32;

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Matches 88; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASLSDRVITTCRASQDINNYLNWYQKPGDGVTKLLIYYTSTLHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGGKLEIKR 108

RESULT 11
KV5L_MOUSE
ID KV5L_MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR: A01927; KVSAR.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFF58E CRC64;

Query Match 41.2%; Score 461; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 1.2e-31;
Matches 88; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASLSDRVITTCRASQDINNYLNWYQKPGDGVTKLLIYYTSTLHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGGKLEIKR 108

RESULT 12
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).

Query Match 41.2%; Score 461; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 1.2e-31;
Matches 88; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASLSDRVITTCRASQDINNYLNWYQKPGDGVTKLLIYYTSTLHSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGQGTKEIKR 108
DB 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGGKLEIKR 108

RESULT 13
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUWK.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 41.1%; Score 459; DB 1; Length 108;
Best Local Similarity 81.5%; Pred. No. 1.8e-31;
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSSLSASVGRVITTCRASQSYNYVAFQKPGKAPKLLIYDASTLQSGVPS 60
QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGNLTPPTFGQGTKEIKR 108
DB 61 NFGSGSGTDFLTITISLPEDFATYYCQYNSPYTFGQGTKEIKR 108

RESULT 13
KVIV_HUMAN
ID KVIV_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1HUWK.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig. 1.  
DR SMART: SM00406; IGV: 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 46 56 FRAMEWORK-2.  
FT DOMAIN 57 71 FRAMEWORK-3.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;  
  
Query Match 41.1%; Score 459; DB 1; Length 129;  
Best Local Similarity 84.1%; Pred. No. 2.2e-31;  
Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60  
Db 23 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60  
QY 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQOGNTLPTFGQGTKEIK 107  
Db 83 RFSGSGSGTDYTLTISSLOPEDFATYYCQOGNTLPTFGQGTKEIK 129  
  
RESULT 14  
KVLP_HUMAN STANDARD; PRT; 108 AA.  
AC P01597;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region DEE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72053133; PubMed=5124396;  
RA Milstein C.P., Deverson E.V.;  
RT "The amino acid sequence of a human kappa light chain.";  
RL Biochem. J. 123:945-958(1971).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
DR PIR: A01865; KIHUDE.  
DR HSSP: P01607; 1REI.  
DR InterPro: IPR003006; Ig_MHC.  
DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig. 1.  
DR SMART: SM00406; IGV: 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;  
  
Query Match 40.8%; Score 456; DB 1; Length 108;  
Best Local Similarity 79.6%; Pred. No. 3.1e-31;  
Matches 86; Conservative 8; Mismatches 14; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60  
Db 23 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60  
QY 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQOGNTLPTFGQGTKEIK 108  
Db 83 RFSGSGSGTDYTLTISSLOPEDFATYYCQOGNTLPTFGQGTKEIK 129  
  
RESULT 15  
KVLP_HUMAN STANDARD; PRT; 108 AA.  
AC P01608;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Roy.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=68362076; PubMed=55951110;  
RA Hilschmann N.;  
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967))."  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.  
DR PIR: A01874; KIHURY.  
DR HSSP: P80362; 1WTL.  
DR InterPro: IPR003006; Ig_MHC.  
DR InterPro: IPR003596; Ig_v.  
DR Pfam: PF00047; Ig. 1.  
DR SMART: SM00406; IGV: 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;  
  
Query Match 40.8%; Score 456; DB 1; Length 108;  
Best Local Similarity 81.5%; Pred. No. 3.1e-31;  
Matches 88; Conservative 8; Mismatches 12; Indels 0; Gaps 0;  
  
QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60  
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60  
QY 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQOGNTLPTFGQGTKEIK 108  
Db 61 RFSGSGSGTDYTLTISSLOPEDFATYYCQOGNTLPTFGQGTKEIK 108  
  
Search completed: August 14, 2002, 11:07:34  
Job time: 379 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: August 14, 2002, 11:07:12 ; Search time 46.4 Seconds

(without alignments)

797.865 Million cell updates/sec

Title: US-09-811-384-11

Perfect score: 1118

Sequence: 1 DIQMTQSPSSLSASVGRVT.....EVTHQGLSSPVTKSFNRGEC 214

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTEMBL_19:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	794	71.0	234	11 Q9LWF8	Q9LWF8 mus musculus
2	784	70.1	233	11 Q9LWS9	Q9LWS9 mus musculus
3	742	66.4	214	11 Q9RLA5	Q9RLA5 mus musculus
4	701.5	62.7	238	11 Q9NM37	Q9NM37 mus musculus
5	701	62.7	211	11 Q9LXL0	Q9LXL0 mus musculus
6	689.5	61.7	235	11 Q9LW12	Q9LW12 mus musculus
7	474	42.4	108	4 Q9UL77	Q9UL77 homo sapien
8	470.5	42.1	107	4 Q9LSA9	Q9LSA9 homo sapien
9	467	41.8	108	4 Q9UL70	Q9UL70 homo sapien
10	466	41.7	116	4 Q9GPF6	Q9GPF6 homo sapien
11	451	40.3	108	4 Q9UL79	Q9UL79 homo sapien
12	449.5	40.2	107	4 Q9UL81	Q9UL81 homo sapien
13	410	35.7	298	11 Q9QYF0	Q9QYF0 mus musculus
14	404.5	36.2	236	4 Q9E5E1	Q9E5E1 homo sapien
15	403	36.0	109	11 Q920E6	Q920E6 mus musculus
16	391	35.0	107	11 Q9JL84	Q9JL84 mus musculus

17	382	34.2	108	4 Q9UL83	Q9UL83 homo sapien
18	379.5	33.9	109	4 Q9UL85	Q9UL85 homo sapien
19	378.5	33.9	235	11 Q99M11	Q99M11 mus musculus
20	371.5	33.2	109	4 Q9UL78	Q9UL78 homo sapien
21	368.5	33.0	233	11 Q9LV32	Q9LV32 m adult mal
22	366	32.7	111	11 Q920E9	Q920E9 mus musculus
23	359.5	32.2	233	4 Q9E1G9	Q9E1G9 homo sapien
24	358	32.0	127	11 Q925S9	Q925S9 mus musculus
25	357.5	32.0	109	4 Q9UL86	Q9UL86 homo sapien
26	352.5	31.5	241	11 Q92IA6	Q92IA6 mus musculus
27	347	31.0	107	11 Q9ER29	Q9ER29 mus musculus
28	346	30.9	101	11 Q9JL78	Q9JL78 mus musculus
29	340.5	30.5	106	5 Q9U410	Q9U410 schistosoma
30	340	30.4	99	11 Q9JL74	Q9JL74 mus musculus
31	338	30.2	114	4 Q9UL80	Q9UL80 homo sapien
32	313	28.0	97	11 Q9JL76	Q9JL76 mus musculus
33	313	28.0	103	11 Q9JL80	Q9JL80 mus musculus
34	308.5	27.6	104	11 Q9JL82	Q9JL82 mus musculus
35	302	27.0	109	6 Q9N0W5	Q9N0W5 oryctolagus
36	232	20.8	218	11 Q925S1	Q925S1 mus musculus
37	229	20.5	107	4 Q9UL82	Q9UL82 homo sapien
38	226.5	20.3	108	4 Q96SB0	Q96SB0 homo sapien
39	225.5	20.2	107	4 Q9NSD6	Q9NSD6 homo sapien
40	225	20.1	130	11 Q9D8W4	Q9D8W4 mus musculus
41	217	19.4	116	4 Q96JD0	Q96JD0 homo sapien
42	212.5	19.0	112	4 Q96JD1	Q96JD1 homo sapien
43	212	19.0	112	4 Q96JD2	Q96JD2 homo sapien
44	205.5	18.4	130	4 Q9NP29	Q9NP29 homo sapien
45	193	17.3	509	11 Q9QX57	Q9QX57 mus musculus

ALIGNMENTS

RESULT 1					
Q9LWF8					
ID Q9LWF8	PRELIMINARY;	PRT;	234 AA.		
AC Q9LWF8;					
DT 01-DEC-2001 (Tremblrel. 19, Created)					
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)					
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)					
DE HYPOTHETICAL 25.9 KDA PROTEIN.					
OS Mus musculus (Mouse).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX NCBI_taxid=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=COLON;					
RA Strausberg R.;					
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.					
DR EMBL; BC015292; AAH15292.1; -					
KW Hypothetical protein.					
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;					

Query Match	71.0%;	Score 794;	DB 11;	Length 234;
Best Local Similarity	69.6%;	Pred No. 2,7e-65;		
Matches 149;	Conservative 26;	Mismatches 39;	Indels 0;	Gaps 0;
Qy 1	DIQMTQSPSSLSASVGRVITTCRASQDINNNYQQKPKAPKLLIYYTTLHSGVPS 60			
	: : : : : : : : :			
Db 21	DIQMTQTSSLSASVGRVITTCRASQDINNNYQQKPKAPKLLIYYTTLHSGVPS 80			
Qy 61	RFGSGSGTDTLTITSSLPEDFATYCCQGNLTPTFGQGTKEIKRTVAAPSVFIFPP 120			
	: : : : : : : : :			
Db 81	RFGSGSGTDTLTITSSLPEDFATYCCQGNLTPTFGQGTKEIKRTVAAPSVFIFPP 140			
Qy 121	SDEQLKCTASVVCVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSYLSSTLT 180			
	: : : : : : : : :			
Db 141	SSEQTSGASVVCVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSYLSSTLT 200			
Qy 181	LSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC 214			

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Db      201 LTKDEYERHNSYTC EATHKTKTSTPIVKSFNREC 234
      1:1 :11:1 1 11 11: :11: 11111 11

RESULT 2
Q91WS9
ID      Q91WS9      PRELIMINARY;      PRT;      233 AA.
AC      Q91WS9;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-COLON:
RA      Strausberg R.;
RL      Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC013496; AAH13496.1; -.
KW      Hypothetical protein.
FT      NON_TER
FT      NON_TER
SQ      SEQUENCE      233 AA;      25781 MW;      BIC184DA149A16EB CRC64;

Query Match      70.1%;      Score 784;      DB 11;      Length 233;
Best Local Similarity 69.6%;      Pred. No. 2.3e-64;
Matches 149;      Conservative 23;      Mismatches 42;      Indels 0;      Gaps 0;

QY      1 DIQMTQSPSSLSASVSGDRVTITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db      20 DIQMTQTSSLSGLSDRVITSCSGSIANLYNWYQKPGDGVTKLLIYTSLSLHSGVPS 79
      111111: 111111: 111111: 1111111111 1111111111 111111111111
QY      61 RFSSGSGSDTYLTITSLQPEDFATYTCQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
      1111111111111111: 1111111111 1111111111 1111111111 1111111111
Db      80 RFSSGSGSDTYLTISLNEPDIATYTCQYRYLPWTFGGKLEIKRADAAPTVSIFPP 139
      1111111111111111: 1111111111 1111111111 1111111111 1111111111
QY      121 SDEQKSGTASVCLLNFPYREAKVQWVDNALQSGNSQESVTEQDSKDSYSLSSPLT 180
      1111111111111111: 1111111111 1111111111 1111111111 1111111111
Db      140 SSEQLTSGGASVGVCLNFPKDNVKKIDGSRQNGVLNSWTDQDSKDSYSSMSSTLT 199
      1111111111111111: 1111111111 1111111111 1111111111 1111111111
QY      181 LSKADYEKKHYIACEVTHQGLSSPVTKSFNRGEC 214
      1:1 :11:1 1 11 11: :11: 11111 11
Db      200 LTKDEYERHNSYTC EATHKTKTSTPIVKSFNREC 233
      1:1 :11:1 1 11 11: :11: 11111 11

RESULT 3
Q9RIA5
ID      Q9RIA5      PRELIMINARY;      PRT;      214 AA.
AC      Q9RIA5;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE      01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE      KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT      "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT      antibody (Mab 7, its light and heavy chains) and construction of a
RT      single chain antibody (scFv).";
RL      Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF152371; AAD40242.1; -.
DR      HSSP; P01679; 2FBJ
DR      InterPro; IPR003600; Ig_like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig; 2.

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Db 80 SCVPDRFSGSGTDTFTLKISRAVEADLGYYVFCQSHVPTFTGSGTKLEIKRADAAPTV 139
QY 116 FIFPDSDEQLKSGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 175
Db 140 SIFPPSSEQLTSGGASVGVFLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSTM 199
QY 176 SSTLTSLKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 200 SSTLTLDKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238

RESULT 5
Q91XL0 PRELIMINARY; PRT; 211 AA.
AC Q91XL0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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```
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 62.7%; Score 701; DB 11; Length 211;
Best Local Similarity 63.0%; Pred. No. 8.8e-57;
Matches 133; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 4 MTQSPSLSASVGDRTVITCRASODINNNYLNWYQKPKAPKLLIYYTSLHSGVPSRF 63
Db 1 MTQSPASLSVSVGETVTITCRASENIYSLNLAWYQKQKSPOLLVYAATNLADGVPSRF 60

QY 64 GSGGTDYTLTSSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPPSDE 123
Db 61 GSGGTQYSLKINSLOSEDFSGYFCQHEWGPRTFGGKTLEIKRADAAPTVSIFFPSSE 120

QY 124 QLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSK 183
Db 121 QLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSSSTLTLT 180

QY 184 ADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 181 DEYERHNSYTCEATHKTSTSPIVKSFNRNEC 211

RESULT 6
Q91WL2 PRELIMINARY; PRT; 235 AA.
AC Q91WL2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5B8FEF CRC64;

Query Match 61.7%; Score 689.5; DB 11; Length 235;
Best Local Similarity 61.0%; Pred. No. 1.2e-55;
Matches 130; Conservative 33; Mismatches 49; Indels 1; Gaps 1;

QY 2 IQMTQSPSSLSASVGDRTVITCRASODINNNYLNWYQKPKAPKLLIYYTSLHSGVPSR 61
Db 24 IVLQSPAIMSASPCERVMTWCSSSSV-SHHHWYQQKSGTSPKRWIYDTFKLTSGVDR 82

QY 62 FSGSGGTDTYTLTSSLOPEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPPS 121
Db 83 FSGSGGTSLTISNMEADVAIYYCQOWSRNPPTFGVGTKEIKRADAAPTVSIFFPS 142

QY 122 DEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLT 181
Db 143 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSSSTLT 202

QY 182 SKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC 214
Db 203 TKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 7
Q9UL77
```



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ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 42.4%; Score 474; DB 4; Length 108;
Best Local Similarity 85.2%; Pred. No. 2.9e-36;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGSYSTSTL--TFGGGTKVEIKR 108
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQGSYSTSTL--TFGGGTKVEIKR 108

RESULT 8
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Addresson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

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Query Match 42.1%; Score 470.5; DB 4; Length 107;
Best Local Similarity 87.2%; Pred. No. 6.1e-36;
Matches 95; Conservative 5; Mismatches 6; Indels 3; Gaps 2;

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QY 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGSYSTSTL--TFGGGTKVEIKR 108
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQGSYSTSTL--TFGGGTKVEIKR 108

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 41.8%; Score 467; DB 4; Length 108;
Best Local Similarity 84.3%; Pred. No. 1.3e-35;
Matches 91; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60

QY 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGSYSTSTL--TFGGGTKVEIKR 108
Db 61 RFGSGSGTDFTLTISSLQPEDFATYYCQGSYSTSTL--TFGGGTKVEIKR 108

RESULT 10
Q96PF6 PRELIMINARY; PRT; 116 AA.
ID Q96PF6;
AC Q96PF6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:

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RT contributions of Ig V(L) germ line gene use and clonal plasma cell
burden.";
RL Blood 98:714-720(2001).
DR EMBL: AF361758; AAK51465.1; -
FT NON_TER 1
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 41.7%; Score 466; DB 4; Length 116;
Best Local Similarity 78.4%; Pred. No. 1.7e-35;
Matches 91; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

QY 61 RFSGSGSDTYLTISSLQPEDFATYYCQCGNTLPPPTFGQGTKEIKRTVAAPSVF 116

Db 61 RFSGSGSATNFTVITISLQPEDFATYYCQYVHLLPFTFGPGTKVDFKRTVAAPSVF 116

RESULT 11

Q9UL79 PRELIMINARY; PRT; 108 AA.

AC Q9UL79;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION

DE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035035; AAD56271.1; -

DR HSSP: P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 108

FT NON_TER 108

SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 40.3%; Score 451; DB 4; Length 108;

Best Local Similarity 81.5%; Pred. No. 3.8e-34;

Matches 88; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

QY 61 RFSGSGSDTYLTISSLQPEDFATYYCQCGNTLPPPTFGQGTKEIKR 108

Db 61 RFSGSGSDTYLTISLQPEDFATYYCQYYSFPPTFGQGTKEIKR 108

RESULT 12

Q9UL81 PRELIMINARY; PRT; 107 AA.

AC Q9UL81;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION

DE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RA Young D.C.;

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RT fetus.";

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035033; AAD56269.1; -

DR HSSP: P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

FT NON_TER 107

FT NON_TER 107

SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 40.2%; Score 449.5; DB 4; Length 107;

Best Local Similarity 82.4%; Pred. No. 5.2e-34;

Matches 89; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60

QY 61 RFSGSGSDTYLTISSLQPEDFATYYCQCGNTLPPPTFGQGTKEIKR 108

Db 61 RFSGSGSDTYLTISLQPEDFATYYCQSYS-ALTFGPGTKVDIR 107

RESULT 13

Q9QYF0 PRELIMINARY; PRT; 298 AA.

AC Q9QYF0;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE CN 8 SCFV.

DE CN 8.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RP STRAIN=BALE/C; TISSUE=SPLEEN;

RP MEDLINE=20183931; PubMed=10706631;

RA Shinozaki N., Demura T., Fukuda H.;

RT "Isolation of a vascular cell wall-specific monoclonal antibody

RT recognizing a cell polarity by using a phase display subtraction

RT method.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).

DR EMBL: AB036341; BAA88633.1; -

DR HSSP: P01607; IREI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_v.

DR Pfam: PF00047; Ig; 2.

DR SMART: SM00406; IGV; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 36.7%; Score 410; DB 11; Length 298;

Best Local Similarity 59.0%; Pred. No. 8.7e-30;

Matches 85; Conservative 15; Mismatches 26; Indels 18; Gaps 2;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 11:00:45 ; Search time 54.11 Seconds
(without alignments)
439.286 Million cell updates/sec

Title: US-09-811-384-11

Perfect score: 1118

Sequence: 1 DIQMTQSPSSLSASVGRVT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	214	AAW34504	Light chain of hum
2	1118	100.0	214	AAW34506	Light chain of ful
3	1118	100.0	214	AAW08754	Human antibody huH
4	1118	100.0	214	AAW95615	Humanized anti-CD1
5	1118	100.0	214	AAW30632	Recombinant humani
6	1118	100.0	214	AAW66777	rhumaB CD18 light
7	1118	100.0	233	AAW30777	pH52-9.0 humanised
8	1118	100.0	237	AAW95622	psi130 expression
9	1118	100.0	237	AAW30634	Recombinant humani
10	1118	100.0	237	AAW66784	Protein encoded by
11	1118	100.0	537	AAW03664	Anti-CD18 antibody

12	1089	97.4	214	14	AAW43338	Completely humanis
13	1089	97.4	214	19	AAW49815	Amino acid sequenc
14	1069	95.6	367	21	AAV55078	Single chain Fv pr
15	1069	95.6	626	21	AAV55081	Single chain Fv pr
16	1068	95.5	237	19	AAW70703	Protein encoded by
17	1035	92.6	214	14	AAW30776	H52L6-158 murine a
18	1032.5	92.4	237	21	AAW96298	Human IGFAM-10 imm
19	1031	92.2	237	13	AAW24047	Light chain of 4D5
20	1031	92.2	513	22	AAW82924	Anti-HER2 Humab4D5
21	1031	92.2	698	20	AAW83493	4D5 Fab molecule e
22	1029	92.0	214	21	AAW93735	The kappa chain of
23	1028.5	92.0	237	21	AAW96289	Human IGFAM-1 immu
24	1026	91.8	240	22	AAW63665	Amino acid sequenc
25	1024	91.6	214	17	AAW00373	Anti-CD18 chimeric
26	1024	91.6	234	12	AAW13050	CD4-specific CDR-g
27	1021	91.3	238	18	AAW13563	Humanised anti-L-s
28	1018	91.1	236	21	AAW96297	Human IGFAM-9 immu
29	1016.5	90.9	237	21	AAW96301	Human IGFAM-13 imm
30	1016	90.9	218	20	AAW95658	Mus musculus anti-
31	1016	90.9	218	21	AAW85200	Mus musculus anti-
32	1016	90.9	218	22	AAW76947	Light chain amino
33	1015	90.8	234	18	AAW10233	Full variable ligh
34	1014	90.7	233	13	AAW22754	TF8-5G9 CDR-grafte
35	1014	90.7	238	21	AAW90930	Reshaped CAMPATH-1
36	1013	90.6	218	20	AAW95669	Humanised anti-Fas
37	1013	90.6	218	20	AAW95664	Mus musculus anti-
38	1013	90.6	218	22	AAW47087	Mus musculus anti-
39	1013	90.6	218	22	AAW76949	Anti-IgE antibody,
40	1013	90.6	218	22	AAW76951	Full length light
41	1013	90.6	218	22	AAW76953	Full length light
42	1013	90.6	218	22	AAW76958	Variable light cha
43	1013	90.6	238	21	AAW90932	Humanised anti-Fas
44	1011	90.4	214	20	AAW08600	Humanised anti-Fas
45	1011	90.4	218	20	AAW50030	JP11127855 Seq ID
						Human E27 anti-IgE

ALIGNMENTS

RESULT 1	
AAW34504	
ID AAW34504 standard; protein; 214 AA.	
XX AC AAW34504;	
XX AC	
DT 19-MAR-1998 (first entry)	
DE Light chain of humanised H52 antibody.	
XX Humanised antibody; HuH52; light chain; focal ischaemic stroke; embolism;	
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;	
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;	
KW systemic hypoperfusion; cardiac arrest.	
XX Synthetic.	
OS Homo sapiens.	
OS Mus sp.	
XX WO9726912-A2.	
XX PD 31-JUL-1997.	
XX PF 11-JAN-1997; 97WO-US00492.	
XX PR 23-JAN-1996; 96US-0589982.	
XX PA (GETH) GENENTECH INC.	
XX PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.	
XX PI Bednar MW, Gross CE, Thomas GR;	
XX WPI; 1997-393373/36.	
XX	

PT Administering an anti-CD18 antibody to treat focal ischaemic stroke
PT - by increasing cerebral blood flow and reducing size of brain
XX infarct
XX
PS Disclosure; Page 9; 41pp; English.
XX
CC This sequence represents the light chain of the humanised H52 antibody.
CC The H52 antibody can be used in the method of the invention. The method
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
CC interrupted blood supply, in a mammal, caused by obstruction of a main
CC cerebral artery, comprises administering anti-CD18 antibody to increase
CC cerebral blood flow and/or reduce the size of the area of brain that
CC dies, without removing the arterial obstruction. CD18, is upregulated in
CC patients after ischaemic stroke or transient ischaemic attack (stroke
CC symptoms last less than 24 hours with complete recovery). Treatment with
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
CC infarct size, improving clinical outcomes in focal ischaemic strokes in
CC mammals, particularly in humans. The method provides an alternative to
CC thrombolytic therapy for treating ischaemic strokes caused by
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
CC therapy has been unsuccessful, is contra-indicated e.g. because such
CC drugs exacerbate bleeding, or is unsuitable because of the time delay
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
CC plasminogen activator) may also be administered before, after or
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
CC be used to treat the third main type of ischaemic stroke, systemic
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 18; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Dy 1 diqmtqspsslsasvgdrtvitcrasqdinnlynwqqkpgkapklliyystlshgvp 60
Qy 61 RFSGSGGTDYTLTSSIQPEDFATYVCOQGNTPPTFGGKVEIKRTVAAPSVFIIPP 120
Dy 61 rfsdgsdtdytltsisqpedfatyvcqgntlptfggkveikrtvaapsvfifpp 120
Qy 121 SDEQLKSGTASVYVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLT 180
Dy 121 sdeqlksgtasvyclnnfyprcakvqwkvdnalqsgnsqesvteqdsksdstylsstlt 180

Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Dy 181 lskadyekhkvayacevthqglsspvtksfnrgec 214

RESULT 2
AAW34506
ID AAW34506 standard; protein; 214 AA.
XX
AC AAW34506;
XX
DT 19-MAR-1998 (first entry)
XX
DE Light chain of full length IgG2 humanised H52 antibody.
XX
KW Humanised antibody; Huh52; light chain; focal ischaemic stroke; embolism;
KW brain damage; anti-CD18 antibody; cerebral blood flow; thromboembolism;
KW transient ischaemic attack; thrombolytic therapy; thrombosis; therapy;
KW systemic hypoperfusion; cardiac arrest.
XX
OS Synthetic.
OS Homo sapiens.
OS Mus sp.
XX
PN W09726912-A2.
XX

PD 31-JUL-1997.
XX
PF 11-JAN-1997; 97WO-US00492.
XX
PR 23-JAN-1996; 96US-0589982.
XX
PA (GETH) GENENTECH INC.
PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
XX
PI Bednar MM, Gross CE, Thomas GR;
XX WPI; 1997-393373/36.
DR Administering an anti-CD18 antibody to treat focal ischaemic stroke
XX - by increasing cerebral blood flow and reducing size of brain
PT infarct
PT
XX Disclosure; Page 10; 41pp; English.
XX
CC This sequence represents the light chain of the humanised H52 antibody.
CC The H52 antibody can be used in the method of the invention. The method
CC is for treating focal ischaemic stroke, i.e. damage to the brain due to
CC interrupted blood supply, in a mammal, caused by obstruction of a main
CC cerebral artery, comprises administering anti-CD18 antibody to increase
CC cerebral blood flow and/or reduce the size of the area of brain that
CC dies, without removing the arterial obstruction. CD18, is upregulated in
CC patients after ischaemic stroke or transient ischaemic attack (stroke
CC symptoms last less than 24 hours with complete recovery). Treatment with
CC anti-CD18 antibodies can increase cerebral blood flow and/or reduce brain
CC infarct size, improving clinical outcomes in focal ischaemic strokes in
CC mammals, particularly in humans. The method provides an alternative to
CC thrombolytic therapy for treating ischaemic strokes caused by
CC thromboembolism (thrombosis or embolism), particularly where thrombolytic
CC therapy has been unsuccessful, is contra-indicated e.g. because such
CC drugs exacerbate bleeding, or is unsuitable because of the time delay
CC between stroke onset and diagnosis. Thrombolytic agents (e.g. tissue
CC plasminogen activator) may also be administered before, after or
CC simultaneously with the anti-CD18 antibody. Alternatively, the method can
CC be used to treat the third main type of ischaemic stroke, systemic
CC hypoperfusion, e.g. resulting from cardiac arrest or drowning.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 18; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQWTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Dy 1 diqmtqspsslsasvgdrtvitcrasqdinnlynwqqkpgkapklliyystlshgvp 60
Qy 61 RFSGSGGTDYTLTSSIQPEDFATYVCOQGNTPPTFGGKVEIKRTVAAPSVFIIPP 120
Dy 61 rfsdgsdtdytltsisqpedfatyvcqgntlptfggkveikrtvaapsvfifpp 120
Qy 121 SDEQLKSGTASVYVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLT 180
Dy 121 sdeqlksgtasvyclnnfyprcakvqwkvdnalqsgnsqesvteqdsksdstylsstlt 180

Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Dy 181 lskadyekhkvayacevthqglsspvtksfnrgec 214

RESULT 3
AAW08754
ID AAW08754 standard; protein; 214 AA.
XX
AC AAW08754;
XX
DT 10-AUG-1999 (first entry)
XX

DE Human antibody huH52 light chain protein fragment.
 XX IgG4; immunoglobulin G; CH1 domain; human; anti-CD18; IgG1; IgG2; IgG3;
 KW IgG4; Kappa-CL domain; lambda-CL domain; focal ischaemic stroke;
 KW cerebroprotective; cerebral artery obstruction; blood flow; infarct;
 KW CD18 extracellular domain; endothelium; CD11b/CD18 complex dissociation;
 KW antibody; huH52; light chain.
 XX Homo sapiens.
 OS
 XX US5914112-A.
 PN
 XX 22-JUN-1999.
 PD
 XX 22-JAN-1997; 97US-0788800.
 PF
 XX 23-JAN-1996; 96US-0093038.
 PR
 XX 22-JAN-1997; 97US-0788800.
 PR
 XX (GETH) GENENTECH INC.
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 PA Bednar MM, Gross CE, Thomas GR;
 PI WPI; 1999-370483/31.
 XX
 XX Anti-CD18 antibodies in stroke
 PT
 XX Claim 11; Column 31-32; 25pp; English.
 PS
 XX This invention describes a method for improving the clinical outcome in
 CC focal ischaemic stroke by administering novel anti-CD18 antibody which
 CC has cerebroprotective properties. The invention particularly describes a
 CC method of treating focal ischemic stroke caused by the obstruction of a
 CC main cerebral artery which comprises administering an anti-CD18 antibody
 CC to increase the blood flow or reduce the infarct size, where: (1) the
 CC antibody binds to an extracellular domain of CD18 and inhibits or reduces
 CC the ability of the cell expressing CD18 to bind to endothelium, (2) the
 CC antibody binds CD18 with an affinity of less than 4 nm, or (3) the
 CC antibody dissociates CD18/CD18 complex. This sequence represents the
 CC human antibody huH52 light chain region.
 XX
 XX Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 20; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2.4e-56;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASODINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
 Db 1 diqmtqspsslsasvgrvritcrasqdinnylnwyqkpgkapklliytytstlhsgvps 60
 QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSVEIFPP 120
 Db 61 rfsgsgsgtdytltlisslpedfatyyccgqgntlpptfgggtkveikrtvaapsvfifpp 120
 QY 121 SDEQLKSGTASVVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
 Db 121 sdeqlksgtasvvccllnfypreakvqkvdnalqsgnsqesvteqdsksdystlsstlt 180
 QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
 Db 181 lskadyekkhkyacevthqglsspvtksfnrgec 214

RESULT 4
 AAW95615
 ID AAW95615 standard; protein; 214 AA.
 XX
 AC AAW95615;
 XX
 DT 08-JUN-1999 (first entry)

XX Humanized anti-CD18 antibody rhuMAB CD18 light chain.
 DE
 XX Monoclonal antibody; heavy chain; humanized; myocardial infarction;
 KW burns; thermal injury; ischemic; shock; ischaemic; haemorrhagic;
 KW hemorrhagic; stroke.
 XX Mus musculus.
 OS
 XX Synthetic.
 OS
 XX WO9856418-A1.
 PN
 XX 17-DEC-1998.
 PD
 XX 12-JUN-1998; 98WO-US12209.
 PF
 XX 13-JUN-1997; 97US-0874897.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z;
 PI Wang SX, Weissburg RP, Wong RL;
 PI WPI; 1999-080860/07.
 XX
 XX New stable aqueous antibody formulations - comprising an antibody
 PT not subjected to lyophilisation, a buffer maintaining the pH at 4.5
 PT - 6, a surfactant and a polyol
 PT
 XX Disclosure; Fig 1B; 87pp; English.
 PS
 XX The sequence is that of the heavy chain of a humanized murine
 CC anti-CD18 antibody rhuMAB CD18. It can be used for the treatment
 CC of disorders which include haemorrhagic shock, thermal injury (such
 CC as that resulting from burns), stroke (including ischaemic and
 CC haemorrhagic stroke) and myocardial infarction. The antibody
 CC formulation can be stabilised at a temperature of 2-8 deg. C
 CC for at least one year or at a temperature of 30 deg. C for at
 CC least one month and is stable following freezing and thawing.
 XX
 XX Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 20; Length 214;
 Best Local Similarity 100.0%; Pred. No. 2.4e-56;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGRVTITCRASODINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
 Db 1 diqmtqspsslsasvgrvritcrasqdinnylnwyqkpgkapklliytytstlhsgvps 60
 QY 61 RFSGSGSGTDYTLTISSLPEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSVEIFPP 120
 Db 61 rfsgsgsgtdytltlisslpedfatyyccgqgntlpptfgggtkveikrtvaapsvfifpp 120
 QY 121 SDEQLKSGTASVVCLLNFPYPRKAVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
 Db 121 sdeqlksgtasvvccllnfypreakvqkvdnalqsgnsqesvteqdsksdystlsstlt 180
 QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
 Db 181 lskadyekkhkyacevthqglsspvtksfnrgec 214

RESULT 5
 AAW30632
 ID AAW30632 standard; protein; 214 AA.
 XX
 AC AAW30632;
 XX
 DT 06-APR-1999 (first entry)
 XX
 DE Recombinant humanised anti-CD18 antibody rhuMAB CD18 light chain.

XX Recombinant humanised anti-CD18 antibody; rhuMAB CD18; leucine zipper;
KW murine monoclonal antibody; muMAB H52; protein recovery; filtration;
KW chromatography.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
PN W09856808-A1.
XX
XX 17-DEC-1998.
PD
XX 12-JUN-1998; 98WO-US12334.
PF
XX 13-JUN-1997; 97US-0050951.
PR
XX (GETH) GENENTECH INC.
PA
XX Blank GS, Narindray DS, Zapata GA;
PI
XX WPI; 1999-060267/05.
DR
XX New method for recovering polypeptides from cell cultures - by
PT treating with reagent and filtering to remove reagent
PT
XX
PS Example; Fig 1B; 43pp; English.
XX
XX A method has been developed for recovering a polypeptide comprising: (a)
CC exposing a composition comprising a polypeptide to a reagent which binds
CC to or modifies the polypeptide, where the reagent is immobilized on a
CC solid phase; and (b) passing the composition through a filter bearing an
CC opposite charge to the reagent so as to remove leached reagent from the
CC composition. The present invention also describes a method for modifying
CC a precursor antibody comprising a leucine zipper by exposing the
CC precursor antibody to a protease immobilized on a solid support so that
CC the protease removes the zipper. The methods can be used to purify
CC proteins from cell cultures. They are especially useful for isolating
CC antibodies. The methods overcome the problem of reagent leakage into the
CC protein as is the case in prior art immobilized modification systems. By
CC using a opposite charge filter the reagent can be excluded from the
CC sample, preventing contamination. The present sequence represents the
CC recombinant humanised anti-CD18 antibody (rhuMAB CD18) light chain,
CC which is used in an example from the present invention.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 20; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 diqmtqspsslsasvgdrtvitcrasqdinnylnwyyqkpgkapklliyystlshsgvps 60
Qy 61 RFGSGSGTDYTLTISSLOPEFATYVCOQGNLPTPTFGQGTVEIKRTVAAPSVFIAPP 120
Db 61 rfsgsgsgtdytltlsslpdefatyvcoqgnltptfpggtkveikrtvaapsvfifpp 120
Qy 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSLSSTLT 180
Db 121 sdeqlksgtasvclnnfyprcakvqkwvdnalsqnsqesvteqdsksdystylsstlt 180
Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 lskadyekhkvacevthqglsspvtksfnrgec 214

RESULT 6
AAB66777
ID AAB66777 standard; protein; 214 AA.
XX

AAB66777;
XX 10-APR-2001 (first entry)
XX
XX rhuMAB CD18 light chain.
XX
XX Antibody; lyophilization; hemorrhagic shock; thermal injury;
KW myocardial infarction; inflammation.
XX
XX Homo sapiens.
XX
XX US6171586-B1.
PN
XX 09-JAN-2001.
PD
XX 12-JUN-1998; 98US-0097171.
PF
XX 13-JUN-1997; 97US-0053087.
PR
XX (GETH) GENENTECH INC.
PA
XX
XX Lam XM, Oeswein JO, Ongpipattanakul B, Shahrokh Z, Wang SX;
PI Weissburg RP, Wong RL;
PI
XX WPI; 2001-136863/14.
DR
XX
XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
PT shock, thermal injury, stroke, and myocardial infarction, comprises an
PT antibody not subjected to prior lyophilization -
PT
XX Example 1; Fig 1; 56pp; English.
XX
XX The present invention relates to a stable aqueous pharmaceutical
CC formulation, comprising an antibody not subjected to prior
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
CC a polyol. The invention is useful for treating hemorrhagic shock,
CC thermal injury, e.g. resulting from burns, stroke including
CC ischemic and hemorrhagic stroke, myocardial infarction,
CC inflammatory disorders such as adult respiratory distress
CC syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
CC arthritis and B-cell lymphomas.
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 1118; DB 22; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 diqmtqspsslsasvgdrtvitcrasqdinnylnwyyqkpgkapklliyystlshsgvps 60
Qy 61 RFGSGSGTDYTLTISSLOPEFATYVCOQGNLPTPTFGQGTVEIKRTVAAPSVFIAPP 120
Db 61 rfsgsgsgtdytltlsslpdefatyvcoqgnltptfpggtkveikrtvaapsvfifpp 120
Qy 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSLSSTLT 180
Db 121 sdeqlksgtasvclnnfyprcakvqkwvdnalsqnsqesvteqdsksdystylsstlt 180
Qy 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 lskadyekhkvacevthqglsspvtksfnrgec 214

RESULT 7
AAR30777
ID AAR30777 standard; protein; 233 AA.
XX
XX AAR30777;
XX
DT 12-MAY-1993 (first entry)

FT Peptide 1..23
FT /label= signal
PN WO9856808-A1.
XX
XX 17-DEC-1998.
PD
XX
XX 12-JUN-1998; 98WO-US12334.
PF
XX
XX 13-JUN-1997; 97US-0050951.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Blank GS, Narindray DS, Zapata GA;
PI
XX WPI; 1999-060267/05.
DR N-PSDB; AAX03840.
XX
XX New method for recovering polypeptides from cell cultures - by
PT treating with reagent and filtering to remove reagent
PT
XX
XX Example; Fig 4; 43pp; English.
XX
XX A method has been developed for recovering a polypeptide comprising: (a)
CC exposing a composition comprising a polypeptide to a reagent which binds
CC to or modifies the polypeptide, where the reagent is immobilized on a
CC solid phase; and (b) passing the composition through a filter bearing an
CC opposite charge to the reagent so as to remove leached reagent from the
CC composition. The present invention also describes a method for modifying
CC a precursor antibody comprising a leucine zipper by exposing the
CC precursor antibody to a protease immobilized on a solid support so that
CC the protease removes the zipper. The methods can be used to purify
CC proteins from cell cultures. They are especially useful for isolating
CC antibodies. The methods overcome the problem of reagent leakage into the
CC protein as is the case in prior art immobilized modification systems. By
CC using a opposite charge filter the reagent can be excluded from the
CC sample, preventing contamination. The present sequence represents the
CC recombinant humanised anti-CD18 antibody (rhuMAB CD18) light chain,
CC which is used in an example from the present invention.
XX
XX Sequence 237 AA;
SQ

Query Match 100.0%; Score 1118; DB 20; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 24 diqmtqspsslsasvsgdrvtitcrasqdinnylnwyqkpgkapklliiyytstlhsgvps 83
QY 61 RFSGSGGTDYTLTISSLPQEDFATYYCQOGNTLPPTFGQGTVEIKRTVAAPSVFIAPP 120
DB 84 rfsqsgsgtdytltiisslpqedfatyyccqognltpptfgggtkveikrtvvaapsvfifpp 143
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 144 sdeqlksgtasvclnnfyprcakvqkvdnalgsgnsqesvteqdsksdyslsstlt 203
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 lskadyekhyacevthqglsspvtksfnrgec 237

RESULT 10
AAB66784
ID AAB66784 standard; protein; 237 AA.
XX
XX AAB66784;
XX
XX 10-APR-2001 (first entry)
DT
XX
XX Protein encoded by ps 1130 expression cassette.

XX Antibody; lyophilization; hemorrhagic shock; thermal injury;
KW myocardial infarction; inflammation.
XX
XX Homo sapiens.
XX
XX US6171586-B1.
PN
XX
XX 09-JAN-2001.
PD
XX
XX 12-JUN-1998; 98US-0097171.
PF
XX
XX 13-JUN-1997; 97US-0053087.
PR
XX
XX (GETH) GENENTECH INC.
PA
XX
XX Lam XM, Oeswein JQ, Ongpipattanakul B, Shahrokh Z, Wang SX;
PI Weissburg RP, Wong RL;
XX
XX WPI; 2001-136863/14.
DR
XX
XX Stable aqueous pharmaceutical formulation for treating hemorrhagic
PT shock, thermal injury, stroke, and myocardial infarction, comprises an
PT antibody not subjected to prior lyophilization
PT
XX Disclosure; Fig 21; 56pp; English.
XX
XX The present invention relates to a stable aqueous pharmaceutical
CC formulation, comprising an antibody not subjected to prior
CC lyophilization, an acetate buffer of pH 4.8-5.5, a surfactant and
CC a polyol. The invention is useful for treating hemorrhagic shock,
CC thermal injury, e.g. resulting from burns, stroke including
CC ischemic and hemorrhagic stroke, myocardial infarction,
CC inflammatory disorders such as adult respiratory distress
CC syndrome (ARDS), hypovolemic shock, ulcerative colitis, rheumatoid
CC arthritis and B-cell lymphomas.
XX
XX Sequence 237 AA;
SQ

Query Match 100.0%; Score 1118; DB 22; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.6e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQKPGKAPKLLIYYTSTLHSGVPS 60
DB 24 diqmtqspsslsasvsgdrvtitcrasqdinnylnwyqkpgkapklliiyytstlhsgvps 83
QY 61 RFSGSGGTDYTLTISSLPQEDFATYYCQOGNTLPPTFGQGTVEIKRTVAAPSVFIAPP 120
DB 84 rfsqsgsgtdytltiisslpqedfatyyccqognltpptfgggtkveikrtvvaapsvfifpp 143
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 144 sdeqlksgtasvclnnfyprcakvqkvdnalgsgnsqesvteqdsksdyslsstlt 203
QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 lskadyekhyacevthqglsspvtksfnrgec 237

RESULT 11
AAB03664
ID AAB03664 standard; Protein; 537 AA.
XX
XX AAB03664;
AC
XX
XX 04-OCT-2000 (first entry)
DT
XX
XX Anti-CD18 antibody (rhuMAB CD18) light and heavy chain protein sequence.
DE
XX Expression cassette; pSL130; rhuMAB CD18; monoclonal antibody;
KW biochemical lysis; polypeptide recovery; anti-CD18 antibody.
KW

```
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Region 1..248
XX FT /note= "Anti-CD18 light chain"
XX FT Region 249..537
XX FT /note= "Anti-CD18 heavy chain"
XX PN WO200024873-A1.
XX XX
XX PD 04-MAY-2000.
XX XX
XX PF 21-OCT-1999; 99WO-US24696.
XX XX
XX PF 28-OCT-1998; 98US-0106052.
XX XX
XX PA (GETH ) GENENTECH INC.
XX XX
XX PI Leung WS, Swartz JR;
XX XX
XX DR WPI; 2000-350719/30.
XX DR N-PSDB; AAA53339, AAA53389.
XX XX
XX PT Process for large scale production and recovery of polypeptides from
XX PT bacterial cells using a method of biochemical lysis -
XX XX
XX PS Example 1; Fig 4; 64pp; English.
XX XX
XX CC This sequence represents the anti-CD18 antibody (rhumab CD18) light and
XX CC heavy chain amino acid sequences. Rhumab CD18 is a recombinant F(ab')2
XX CC antibody, which binds to the MAC-1 (CD11b/CD18) receptor, blocking
XX CC binding of neutrophils to the endothelium. The expression cassette is
XX CC used in an example of the process of the invention, for recovering a
XX CC heterologous polypeptide from bacterial cells using biochemical lysis.
XX CC The process is used for the large scale production and recovery of
XX CC polypeptides e.g. human insulin-like growth factor (IGF), DNase, vascular
XX CC endothelial growth factor (VEGF), anti-CD18 antibody or anti-CD18
XX CC antibody fragment from bacterial cells.
XX XX
XX SQ Sequence 537 AA;

Query Match 100.0%; Score 1118; DB 21; Length 537;
Best Local Similarity 100.0%; Pred. No. 5.4e-56;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQOKPGKAPKLLIYVTTSLHSGVPS 60
DB 24 diqmtqspsslsasvgrvtitcrasqdinnylnwyqkpgkapklllytstllhsgvps 83
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSFIIPP 120
DB 84 rfsgsgsgtdytlttisslpqedfatyycggntlpptfgggtkveikrtvaapsvfifpp 143
QY 121 SDEQLKSGTASVCLLNFFYPREAKVQWKNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 144 sdeqlksgtasvcllnffypreakvqwkvdnalqsgnsqesvteqgskdstyslsstlt 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 lskadyekhkvyacevthqglsspsvtskfsnrgec 237

RESULT 12
AAR43338
ID AAR43338 standard; Protein; 214 AA.
XX
XX AAR43338;
XX AC
XX AC
XX DT 29-NOV-1993 (first entry)
XX XX
XX DE Completely humanised C4G1 Ig light chain.
```

```
XX XX Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIb;
XX KW monoclonal antibody; platelet agglutination; humanised antibody.
XX OS Synthetic.
XX XX WO9313133-A.
XX PN
XX XX 08-JUL-1993.
XX PD
XX PF 15-DEC-1992; 92WO-JP01630.
XX XX
XX PR 20-DEC-1991; 91US-0812111.
XX PR 09-JUN-1992; 92US-0895952.
XX PR 11-SEP-1992; 92US-0944159.
XX XX
XX PA (PROT-) PROTEIN DESIGN LABS INC.
XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX XX
XX PI Co MS, Tso JY;
XX XX
XX DR WPI; 1993-227275/28.
XX XX
XX PT Compsn. contg. immunoglobulin specific for the GP-IIb and -IIIA
XX PT protein - for treating disorders related to vascular thrombosis
XX PS Claim 26; Fig 5C; 54pp; Japanese.
XX XX
XX CC This is the sequence of the humanised C4G1 immunoglobulin light
XX CC chain fragment. See AAR43339 for the heavy chain sequence. The
XX CC antibody is specific for the platelet membrane glycoprotein
XX CC GPIIa/IIb and inhibits platelet agglutination. The Ig is thus
XX CC useful in the treatment of thrombosis.
XX XX
XX SQ Sequence 214 AA;

Query Match 97.4%; Score 1089; DB 14; Length 214;
Best Local Similarity 96.7%; Pred. No. 1e-54;
Matches 207; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQOKPGKAPKLLIYVTTSLHSGVPS 60
DB 1 diqmtqspsslsasvgrvtitcrasqdinnylnwyqkpgkapklllytstllhsgvps 60
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGGNTLPPTFGQGTKEIKRTVAAPSFIIPP 120
DB 61 rfsgsgsgtdytlttisslpqedfatyycggntlpwtfgggtkveikrtvaapsvfifpp 120
QY 121 SDEQLKSGTASVCLLNFFYPREAKVQWKNALQSGNSQESVTEQDSKDSYSLSTLT 180
DB 121 sdeqlksgtasvcllnffypreakvqwkvdnalqsgnsqesvteqgskdstyslsstlt 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 lskadyekhkvyacevthqglsspsvtskfsnrgec 214

RESULT 13
AAR49815
ID AAR49815 standard; Protein; 214 AA.
XX
XX AC AAR49815;
XX AC
XX DT 24-SEP-1998 (first entry)
XX XX
XX DE Amino acid sequence of the humanised antibody C4G1 light chain.
XX XX
XX KW Humanised antibody C4G1; light chain; humanised; immunoglobulin; Ig;
XX KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
XX KW thromboembolic disorder; cancer; acute myocardial infarction;
XX KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
XX KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
```

```
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX US5777085-A.
XX 07-JUL-1998.
XX 17-MAY-1995; 95US-0458516.
XX 03-MAY-1993; 93US-0059159.
PR 20-DEC-1991; 91US-0812111.
PR 09-JUN-1992; 92US-0895952.
PR 11-SEP-1992; 92US-0944159.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Co MS, Tso JY;
XX WPI; 1998-398136/34.
XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from
PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
PT treating cardiovascular and thromboembolic disorders.
XX Claim 4; Fig 5C; 35pp; English.
XX This is the amino acid sequence of the humanised antibody C4G1 light
CC chain, used in the method of the invention involving the creation
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
CC platelet aggregation and also the releasing reaction of platelets. The
CC Ig can be used for treating cardiovascular diseases and thromboembolic
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets.
XX Sequence 214 AA;
SQ
Query Match 97.4%; Score 1089; DB 19; Length 214;
Best Local Similarity 96.7%; Pred. No. 1e-54;
Matches 207; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQWTQSPSLSASVGRVITICRASQDINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
DB 1 diqmtqtptstlsasvgrvdtiscrasqdinnlnwyqdkpgkapklliytstlshgyps 60
QY 61 RFGSGSGTDYTLTISLQPEDFATYYCQCGNTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
DB 61 rfsgsgsgtdytltisllqpddfatyfcqqgntlpwtfggtkvekrtvaapsvfifpp 120
QY 121 SDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 180
DB 121 sdeqlksgtasvcllnnfyreakvgkvdnalqsgnsqesvteqskdstyslsstlt 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 lskadyekhkvyacevthqglsspvtksfnrgec 214
RESULT 14
AAAY55078
ID AAY55078 standard; Protein; 367 AA.
XX
XX AAY55078;
XX
XX 25-QEB-2000 (first entry)
XX
XX Single chain Fv protein sequence shPM1-kappa.
```

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XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretable functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
XX Synthetic.
OS WO99601113-A1.
PN 25-NOV-1999.
XX 30-APR-1999; 99WO-JP02341.
PF 20-MAY-1998; 98JP-0138652.
XX 01-OCT-1998; 98JP-0279876.
PR 01-OCT-1998; 98JP-0279876.
XX (CHUS ) CHUGAI SEIYAKU KK.
PA Tsuchiya M, Saito M, Ohtomo T;
XX WPI; 2000-039382/03.
XX N-PSDB; AA240308.
DR Efficient and selective isolation of a gene encoding membrane protein
XX with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein -
PT Example 7; Page 86-89; 120pp; Japanese.
XX This sequence represents a single chain Fv (ScFv) sequence.
CC The invention relates to a method for isolating a gene encoding a
CC membrane-bound protein, comprising introducing a vector into a cell,
CC contacting an antigen with the cell expressing the fused protein encoded
CC by the vector on its surface to select an antigen-binding cell, and
CC isolating the cDNA. The vector contains DNA encoding a secretable
CC functional protein with antigenicity and binding affinity, and a cDNA
CC ligated to DNA downstream of the 3' end of the coding sequence. The
CC method can be used to isolate a membrane-bound protein for diagnosis
CC study. It can also be used for producing drugs treating abnormal
CC functions of the protein. Such a technique is efficient and selective,
CC which is different from the prior-art transmembrane trap (TMT) method
CC wherein an epitope recognised by an antibody is carried in a fused
CC protein.
XX Sequence 367 AA;
SQ
Query Match 95.6%; Score 1069; DB 21; Length 367;
Best Local Similarity 96.7%; Pred. No. 2.3e-53;
Matches 206; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIQMTQSPSLSASVGRVITICRASQDINNYLNWYQKPKAPKLLIYYTSTLHSGVPS 60
DB 154 diqmtqspslsasvgrvdtitcrasqdissylnwyyqkpgkapklliytstlrhsgvps 213
QY 61 RFGSGSGTDYTLTISLQPEDFATYYCQCGNTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
DB 61 rfsgsgsgtdytltisllqpddfatyfcqqgntlpytfggtkveikrtvaapsvfifpp 273
QY 121 SDEQLKSGTASVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 180
DB 121 sdeqlksgtasvcllnnfyreakvgkvdnalqsgnsqesvteqskdstyslsstlt 333
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
DB 334 lskadyekhkvyacevthqglsspvtksfnrge 366
RESULT 15
AAAY55081
ID AAY55081 standard; Protein; 626 AA.
XX
XX AAY55081;
AC
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 11:01:12 ; Search time 20.83 seconds
(without alignments)
250.940 Million cell updates/sec

Title: US-09-811-384-11
Perfect score: 1118
Sequence: 1 DIQWSPSLASVGDVTV.....EVTHQGLSSPVTKSFNRGEC 214

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents.AA.*
- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	214	2 US-07-934-373C-40	Sequence 40, Appl
2	1118	100.0	214	2 US-08-788-800-11	Sequence 11, Appl
3	1118	100.0	214	3 US-08-437-642B-40	Sequence 40, Appl
4	1118	100.0	214	3 US-09-097-309-2	Sequence 2, Appl
5	1118	100.0	214	4 US-09-097-171A-2	Sequence 2, Appl
6	1118	100.0	214	5 PCT-US93-07832-40	Sequence 40, Appl
7	1118	100.0	233	2 US-07-934-373C-25	Sequence 25, Appl
8	1118	100.0	233	3 US-08-437-642B-25	Sequence 25, Appl
9	1118	100.0	233	5 PCT-US93-07832-25	Sequence 25, Appl
10	1118	100.0	237	3 US-09-097-309-6	Sequence 6, Appl
11	1118	100.0	237	4 US-09-097-171A-10	Sequence 10, Appl
12	1118	100.0	237	4 US-09-422-712B-2	Sequence 2, Appl
13	1118	100.0	237	4 US-09-607-756-2	Sequence 2, Appl
14	1110	99.3	214	2 US-07-934-373C-39	Sequence 39, Appl
15	1110	99.3	214	3 US-08-437-642B-39	Sequence 39, Appl
16	1110	99.3	214	5 PCT-US93-07832-39	Sequence 39, Appl
17	1089	97.4	214	1 US-08-458-516-12	Sequence 12, Appl
18	1035	92.6	214	2 US-07-934-373C-24	Sequence 24, Appl
19	1035	92.6	214	3 US-08-437-642B-24	Sequence 24, Appl
20	1035	92.6	214	5 PCT-US93-07832-24	Sequence 24, Appl
21	1031	92.2	214	4 US-09-679-397-1	Sequence 1, Appl
22	1031	92.2	237	2 US-08-463-587A-25	Sequence 25, Appl
23	1031	92.2	237	2 US-08-463-667A-3	Sequence 3, Appl
24	1031	92.2	237	3 US-08-923-854-25	Sequence 25, Appl
25	1031	92.2	237	5 PCT-US91-09133-26	Sequence 26, Appl
26	1024	91.6	214	1 US-08-425-763-1	Sequence 1, Appl
27	1024	91.6	214	3 US-08-811-757-1	Sequence 1, Appl

28	1024	91.6	214	4 US-09-249-230-1	Sequence 1, Appl
29	1021	91.3	218	5 PCT-US96-13152-2	Sequence 2, Appl
30	1016	90.9	218	2 US-08-887-352B-13	Sequence 13, Appl
31	1016	90.9	218	3 US-08-466-151-9	Sequence 9, Appl
32	1016	90.9	218	4 US-09-109-207C-13	Sequence 13, Appl
33	1016	90.9	218	4 US-09-296-005-13	Sequence 13, Appl
34	1016	90.9	218	4 US-08-466-163B-9	Sequence 9, Appl
35	1013	90.6	218	2 US-08-887-352B-15	Sequence 15, Appl
36	1013	90.6	218	2 US-08-887-352B-17	Sequence 17, Appl
37	1013	90.6	218	2 US-08-887-352B-19	Sequence 19, Appl
38	1013	90.6	218	2 US-08-887-352B-24	Sequence 24, Appl
39	1013	90.6	218	4 US-09-109-207C-15	Sequence 15, Appl
40	1013	90.6	218	4 US-09-109-207C-17	Sequence 17, Appl
41	1013	90.6	218	4 US-09-109-207C-19	Sequence 19, Appl
42	1013	90.6	218	4 US-09-109-207C-24	Sequence 24, Appl
43	1013	90.6	218	4 US-09-296-005-15	Sequence 15, Appl
44	1013	90.6	218	4 US-09-296-005-17	Sequence 17, Appl
45	1013	90.6	218	4 US-09-296-005-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-40

Query Match 100.0%; Score 1118; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLQPEDFATYYCOQGNLPTTFGGQTKVEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCOQGNLPTTFGGQTKVEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
RESULT 2
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-11

Query Match 100.0%; Score 1118; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLQPEDFATYYCOQGNLPTTFGGQTKVEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCOQGNLPTTFGGQTKVEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180

DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
RESULT 3
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-40

Query Match 100.0%; Score 1118; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
DB 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNNWYQOKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLQPEDFATYYCOQGNLPTTFGGQTKVEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCOQGNLPTTFGGQTKVEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
DB 121 SDEQLKSGTASVCLLNFFYPREKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180

Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYERKHVYACVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACVTHQGLSSPVTKSFNRGEC 214
RESULT 4
US-09-097-309-2
; Sequence 2, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-309-2
Query Match 100.0%; Score 1118; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYYTSTLHSGVPS 60
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Db 61 RFSGSGGTDTLTITSLQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
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Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYERKHVYACVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACVTHQGLSSPVTKSFNRGEC 214
RESULT 5

US-09-097-171A-2
; Sequence 2, Application US/09097171A
; Patent No. 6171586
; GENERAL INFORMATION:
; APPLICANT: Lam, Xanthe M.
; APPLICANT: Oeswein, James Q.
; APPLICANT: Ongpipattanakul, Boonsri
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Wang, Sharon X.
; APPLICANT: Weissburg, Robert P.
; APPLICANT: Wong, Rita L.
; TITLE OF INVENTION: Antibody Formulation
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,171A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874897
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1089R1
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2
Query Match 100.0%; Score 1118; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYYTSTLHSGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNQKPGKAPKLLIYYTSTLHSGVPS 60
QY 61 RFSGSGGTDTLTITSLQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
Db 61 RFSGSGGTDTLTITSLQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIAPP 120
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYERKHVYACVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACVTHQGLSSPVTKSFNRGEC 214
RESULT 6
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

;; TITLE OF INVENTION: Immunoglobulin Variants
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: patin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/07832
;; FILING DATE: 19930820
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/05126
;; FILING DATE: 15-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/934373
;; FILING DATE: 21-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME:
;; REGISTRATION NUMBER:
;; REFERENCE/DOCKET NUMBER: 709P2PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE:
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 214 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
PCT-US93-07832-40

Query Match 100.0%; Score 1118; DB 5; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.5e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
|
Db 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
|
QY 61 RFGSGSGTDYTLTISSIQPEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 120
|
Db 61 RFGSGSGTDYTLTISSIQPEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 120
|
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
|
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
|
QY 181 LSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 214
|
Db 181 LSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 214
|

RESULT 7
US-07-934-373C-25
; Sequence 25, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/934,373C
;; FILING DATE: 21-Aug-1992
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/05126
;; FILING DATE: 15-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709P2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 233 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-07-934-373C-25

Query Match 100.0%; Score 1118; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 60
|
Db 20 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLHSGVPS 79
|
QY 61 RFGSGSGTDYTLTISSIQPEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 120
|
Db 80 RFGSGSGTDYTLTISSIQPEDFATYYCQOGNTLPTTFGGQTKVEIKRTVAAPSVFIFPP 139
|
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
|
Db 140 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 199
|
QY 181 LSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 214
|
Db 200 LSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 233
|

RESULT 8
US-08-437-642B-25
; Sequence 25, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA


```

ZIP:      94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/953-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

```

Query Match	100.0.0%;	Score	1118;	DB	3;	Length	233;
Best Local Similarity	100.0.0%;	Pred. No.	1.17e-88;				
Matches	214;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	DIOMTQSPSSLSASVGDRVTITCRASODINNYLNWYQOKPGKAPKLLIYYTSTLHSGVPS	60				
Db	20	DIOMTQSPSSLSASVGDRVTITCRASODINNYLNWYQOKPGKAPKLLIYYTSTLHSGVPS	79				
QY	61	RFGSGSGDTYTLTISSLQPEDFATYYCQOGNTLPTFGQGTKEVEIKRTVAAPSVFIFPP	120				
Db	80	RFGSGSGDTYTLTISSLQPEDFATYYCQOGNTLPTFGQGTKEVEIKRTVAAPSVFIFPP	139				
QY	121	SDEQLKSGTASVWCLLNFPYREAAKQVQKVDNALQSGNSQESVTEQDSKSTYISLSSTLT	180				
Db	140	SDEQLKSGTASVWCLLNFPYREAAKQVQKVDNALQSGNSQESVTEQDSKSTYISLSSTLT	199				
QY	181	LSKADYEKHKVYACEVTHQGLSSPVTKTSFNRGEC	214				
Db	200	LSKADYEKHKVYACEVTHQGLSSPVTKTSFNRGEC	233				

```

RESULT          9
PCT-US93-07832-25
; Sequence 25, Application PC/TUS9307832
; GENERAL INFORMATION:
;
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genetech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-07832-25

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Query Match	100.0%	Score 1118;	DB 5;	Length 233;
Best Local Similarity	100.0%;	Pred. No. 1.7e-08;		
Matches 214;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DIQMTQSPSSLSASVGDRVTITCRASQDINYNLNWYQOKPKGAPKLLIYYTSTLHSGVPS	60	
Db	20	DIQMTQSPSSLSASVGDRVTITCRASQDINYNLNWYQOKPKGAPKLLIYYTSTLHSGVPS	79	
QY	61	RFSGSGSGTDYTLTISSLPQEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP	120	
Db	80	RFSGSGSGTDYTLTISSLPQEDFATYYCOQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP	139	
QY	121	SDEQLKSGTASVCLLNLFYPREAKVQWKVDNALQSGNSQESVTEQDSKDPSYSLSLTLT	180	
Db	140	SDEQLKSGTASVCLLNLFYPREAKVQWKVDNALQSGNSQESVTEQDSKDPSYSLSLTLT	199	
QY	181	LSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC	214	
Db	200	LSKADYEKHKYVACEVTHQGLSSPVTKSFNRGEC	233	

```

RESULT 10
US-09-097-309-6
; Sequence 6, Application US/09097309
; Patent No. 6121428
;
; GENERAL INFORMATION:
;
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit A.
; APPLICANT: Zapata, Gerardo A.
;
; TITLE OF INVENTION: Protein Recovery
;
; NUMBER OF SEQUENCES: 7
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Genentech, Inc.
;
; STREET: 1 DNA Way
;
; CITY: South San Francisco
;
; STATE: California
;
; COUNTRY: USA
;
; ZIP: 94080
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-Jun-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-309-6

Query Match 100.0%; Score 1118; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 83

QY 61 RFSGSGSGTDYTLTISSLPQDEATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
Db 84 RFSGSGSGTDYTLTISSLPQDEATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVFIFPP 143

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLSTLT 180
Db 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLSTLT 203

QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 11
US-09-097-171A-10
Sequence 10, Application US/09097171A
Patent No. 6171586
GENERAL INFORMATION:
APPLICANT: Lam, Xanthe M.
APPLICANT: Oeswein, James Q.
APPLICANT: Ongpipattanakul, Boonsri
APPLICANT: Shahrokh, Zahra
APPLICANT: Wang, Sharon X.
APPLICANT: Weissburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech),
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-10

Query Match 100.0%; Score 1118; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 83

QY 61 RFSGSGSGTDYTLTISSLPQDEATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
Db 84 RFSGSGSGTDYTLTISSLPQDEATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVFIFPP 143

QY 121 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLSTLT 180
Db 144 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLSTLT 203

QY 181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 12
US-09-422-712B-2
Sequence 2, Application US/09422712B
Patent No. 6180367
GENERAL INFORMATION:
APPLICANT: Leung, Moon-Lam Susan
APPLICANT: Swartz, James R.
TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
FILE REFERENCE: P1711R1
CURRENT APPLICATION NUMBER: US/09/422,712B
CURRENT FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
LENGTH: 237
TYPE: PRT
ORGANISM: Human
US-09-422-712B-2

Query Match 100.0%; Score 1118; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 60
Db 24 DIQMTQSPSSLSASVGDRTVITCRASQDINNLYNWYQKPKAPKLLIYYTSTLHSGVPS 83

QY 61 RFSGSGSGTDYTLTISSLPQDEATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
Db 84 RFSGSGSGTDYTLTISSLPQDEATYYCQOGNTLPPTFGQGTKEIKRTVAAPSVFIFPP 143

QY 121 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 144 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 203
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 13
US-09-607-756-2
; Sequence 2, Application US/09607756
; Patent No. 6258560
; GENERAL INFORMATION:
; APPLICANT: Leung, Woon-Lam Susan
; APPLICANT: Swartz, James R.
; TITLE OF INVENTION: PROCESS FOR BACTERIAL PRODUCTION OF POLYPEPTIDES
; FILE REFERENCE: P1711R1
; CURRENT APPLICATION NUMBER: US/09/607,756
; CURRENT FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/422,712
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Human
US-09-607-756-2

Query Match 100.0%; Score 1118; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCRASQDINNLYNMWYQKPKAPKLLIYTTSLHSGVPS 60
Db 24 DIOMTQSPSSLSASVGDRTVITCRASQDINNLYNMWYQKPKAPKLLIYTTSLHSGVPS 83
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSFIIPP 120
Db 84 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSFIIPP 143
QY 121 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 144 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 203
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 14
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-39

Query Match 99.3%; Score 1110; DB 2; Length 214;
Best Local Similarity 99.5%; Pred. No. 7.4e-88;
Matches 213; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIOMTQSPSSLSASVGDRTVITCRASQDINNLYNMWYQKPKAPKLLIYTTSLHSGVPS 60
Db 1 DIOMTQSPSSLSASVGDRTVITCRASQDINNLYNMWYQKPKAPKLLIYTTSLHSGVPS 60
QY 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSFIIPP 120
Db 61 RFGSGSGTDYTLTISSLPQEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSFIIPP 120
QY 121 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
Db 121 SDEQLKSGTASVWCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 15
US-08-437-642B-39
; Sequence 39, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992

Search completed: August 14, 2002, 11:01:13
Job time: 238 sec